

Scoring table:	BLOSUM62	ALIGMENTS								
Searched:	2166443 seqb, 705528306 residues									
Total number of hits satisfying chosen parameters:	2166443									
Minimum DB seq length:	0									
Maximum DB seq length:	2000000000									
Post-processing:	Minimum Match 0%									
	Maximum Match 10%									
	Listing first 45 summaries									
Database :	UniProt 05.00: 1: uniprot_sprot: 2: uniprot_trembl: *									
<p>^ Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.</p>										
<p>SUMMARIES</p>										
Result No.	Score	Query	Match	Length	DB ID	Description				
1	1827.5	90.6	403	1	S14L2_HUMAN	076054 homo sapien				
2	1824.5	90.4	403	2	Q53EQ2_HUMAN	076052 homo sapien				
3	1726.5	85.6	403	2	Q5EBD0_RAT	05ebd0 rattus norv				
4	1724.5	85.5	403	1	S14L2_MOUSE	099j08 mus musculu				
5	1724.5	85.5	403	2	Q5SQ25_MOUSE	05sqc5 mus musculu				
6	1722.5	85.4	403	1	S14L2_RAT	09gms0 rattus norv				
7	1685.5	83.5	403	2	Q86TA0_BOVIN	086ta0 bos taurus				
8	1616.5	80.1	387	1	S14L2_BOVIN	P58875 bos taurus				
9	1600.5	79.6	392	1	Q6PD61_HUMAN	Q6pd61 homo sapien				
10	1580.5	78.3	401	2	Q5REK6_PONY	Q5rek6 pongo pygma				
11	1428.0	70.8	400	1	S14L3_HUMAN	09qkx4 homo sapien				
12	1426.0	70.7	400	1	Q6XSB2_HUMAN	06isb2 homo sapien				
13	1425.0	70.6	400	2	Q6XC71_HUMAN	06xc17 homo sapien				
14	1413.0	70.0	400	1	S14L3_RAT	09z118 rattus norv				
15	1409.5	69.8	401	2	Q5SQ27_MOUSE	05sqc7 mus musculu				
16	1309.5	64.9	403	1	S14L4_MOUSE	08r019 mus musculu				
17	1309.5	64.9	403	2	Q5SQ22_MOUSE	05sqc22 mus musculu				
18	1304.5	64.6	406	1	S14L4_HUMAN	09udz3 homo sapien				
19	1259.0	62.4	352	2	Q6ICM2_HUMAN	06icm2 homo sapien				
20	1239.0	61.4	389	2	Q4RUZ5_TETNG	04rnz5 tetraodon n				
21	1169.0	57.9	391	2	Q4SIY9_TETNG	04siy9 tetraodon n				
22	661.5	32.8	342	1	RALB_TOIPA	P49193 todarodes p				
23	522.0	25.9	394	2	Q706S7_ANOGA	07q6s7 anopheles g				
24	439.0	21.8	407	2	Q8SYC4_DROME	08sy4 drosophila				
25	433.0	21.5	756	2	Q43304_HUMAN	043304 homo sapien				
26	411.0	20.4	715	2	Q66KK9_XENTR	066kk9 xenopus tro				
27	409.0	20.3	715	2	Q64ID9_XENLA	064id9 xenopus lae				
28	408.0	20.2	383	2	Q17907_CAEFR	017907 caenorhabdi				
29	405.0	20.1	383	2	Q60IR6_CAEFR	060ir6 caenorhabdi				
30	399.0	19.8	681	2	Q8GPB3_XENLA	08gpb3 xenopus lae				
31	397.0	19.7	1	1	S14L1_HUMAN	092503 homo sapien				

Scoring table:	BLOSUM62	ALIGMENTS			
Searched:	2166443 seqb, 705528306 residues				
Total number of hits satisfying chosen parameters:	2166443				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0%				
	Maximum Match 10%				
	Listing first 45 summaries				
Database :	UniProt 05.00: 1: uniprot_sprot: 2: uniprot_trembl: *				
<p>RESULT 1</p> <p>S14L2_HUMAN STANDARD; PRT; 403 AA.</p> <p>ID S14L2_HUMAN AC 07054 ; Q9UIN4; DT 28-FEB-2003 (Rel. 41, Created) DT 28-FEB-2003 (Rel. 41, Last sequence update) DT 13-SEP-2005 (Rel. 48, Last annotation update)</p> <p>DE SEC14-like protein 48 (Alpha-tocopherol-associated protein) (TAPP) (hTAP) (Supernatant protein factor) (SPF) (Squalene transfer protein).</p> <p>DB Name=SEC14L2; Synonyms=KIAA186;</p> <p>OS Homo sapiens (Human).</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.</p> <p>OC Homo' TaxID=9606;</p> <p>OX [1]</p> <p>RN NUCLEOTIDE SEQUENCE (ISOFORM 1), ALTERNATIVE SPlicing, AND RP CHARACTERIZATION.</p> <p>RP Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Saboon J., RA Azzi A.; human tocopherol-associated protein: cloning, in vitro RT expression, and characterization. ";</p> <p>RA RT A novel human tocopherol-associated protein: cloning, in vitro expression, and characterization. ";</p> <p>RL J. Biol. Chem. 275:25652-25680(2000).</p> <p>RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND CHARACTERIZATION.</p> <p>RN TISSUE=Liver; RC MEDLINE=1040504; PubMed=10829015; DOI=10.1074/jbc.M000851200; RX Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Saboon J., RA Yamauchi J., Iwanoto T., Kida S., Matsushige S., Yamada K., Esashi T.; RT "Tocopherol-associated protein is a ligand-dependent transcriptional activator.";</p> <p>RT Bidchem. Biophys. Res. Commun. 285:295-299(2001).</p> <p>RL RN [3]</p> <p>RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND CHARACTERIZATION.</p> <p>RC TISSUE=Liver; RX MEDLINE=1133208; PubMed=11444841; DOI=10.1006/bbrc.2001.5162; RA Shabata N., Arita M., Misaki Y., Dohmae N., Takio K., Ono T., RA Inoue K., Ariai H.; RT "Supernatant protein factor, which stimulates the conversion of squalene to lanosterol is a cytosolic squalene transfer protein and enhances cholesterol biosynthesis.";</p> <p>RL RN [4] Proc. Natl. Acad. Sci. U.S.A. 98:2244-2249(2001).</p> <p>RP NUCLEOTIDE SEQUENCE-[MRNA]--[ISOFORM 1].</p> <p>RA Collins J.E., Huckle-Erds J., Submitted (JUN-1993) to-the-EMBL/GenBank/DBJ_databases..</p> <p>RL RN [5]</p> <p>RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).</p> <p>RX PubMed=15461802; DOI=10.1101/9b-2004-10-78;</p> <p>RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A., Cole C.G., Govard M.B., Aguado B., Mallya M., Mokrab Y., Huckle E.J., RA Bear D.M., Dunham I.; RT "A genome annotation-driven approach to cloning the human ORFeome.";</p> <p>RL RN Genome Biol. 5:RESEARCH04.1-RESEARCH04.11(2004).</p>					

[6]	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RN	Name=3; IsoId=076054-3; Sequence=Not described;
RX	PubMed=10591208; Published: 10-10-1998; DOI=10.1038/990031;	RX	CC TISSUE SPECIFICITY: Widely expressed. Strong expression in liver, brain and prostate.
RA	Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess O.P., Burill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.B., Cole C.G., Collier R.B., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn C., Heathcott R.W., Ho S., Holmes S., Jones M.C., Kerhaw J., Kimberley A.M., King A., Laird G.K., Langford C.F., Levershaw M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccean O.T., McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Philimore B.J.C.T., Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D., Steward C.A., Sulston J.E., Swann R.M., Soderlund C., Spraggon L., Wall M., Wallis J.M., Whitley M.N., Willey D.L., Williams L., Williams S.A., Williamson H., Williamson T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shintani A., Shibusawa K., Yoshizaki Y., Aoki N., Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj B., Nguyen T., Pan H., Lewis S., Qi S., Qian Y., Ray L., Ren Q., Shauil S., Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhang G., Chissoe S., Murray J., Miller N., Mirx P., Fulton R., Johnson D., Bemis G., Bradshaw H., Bourne S., Hordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hands K., Kemp K., Latreille D., Ozerbsky P., Rohlfing T., Scheet P., Kempfer C., Wamsley A., Woldmann P., Pepin K., Neison J., Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurashiki H., Saitta S., Bujard M.L., McDermid H.E., Wong A.C.C., Morrow B.E., Edelman L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyron M., Kedra D., Seroussi E., Fransson T., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tilahun Y., Wright H.; RTR The DNA sequence of human chromosome 22.;	RN	CC TISSUE-BRAIN: PubMed=10574461; MEDLINE=20039618; Name=O;
[7]	NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] OF 191-360 (ISOFORM 2).	RN	CC "Characterization of cDNA clones selected by the Genemarker analysis from size-fractionated cDNA libraries from human brain.";
RT	DNA Res. 6:329-336 (1999).	RT	CC - FUNCTION: Carrier protein. Binds to some hydrophobic molecules and promotes their transfer between the different cellular sites. Binds with high affinity to alpha-tocopherol. Also binds with a weaker affinity to other tocopherols and to tocotrienols. May have a transcriptional activatory activity via its association with alpha-tocopherol. Probably recognizes and binds some squalene structure, suggesting that it may regulate cholesterol biosynthesis by increasing the transfer of squalene to a metabolic active pool in the cell.
RL	QY96102222; Name=3; IsoId=076054-3; Sequence=Displayed;	RL	CC - SUBUNIT: Monomer (BY similarity)
RR	QY96102222; Name=2; IsoId=076054-2; Sequence=VSP_006031;	RR	CC - SUBCELLULAR LOCATION: Cyttoplasmic in absence of alpha-tocopherol, and nuclear in presence of alpha-tocopherol.
CC	QY96102222; Name=1; IsoId=076054-1; Sequence=Displayed;	CC	CC - ALTERNATIVE PRODUCTS:
CC	QY96102222; Name=2; IsoId=076054-2; Sequence=VSP_006031;	CC	CC

Db	1	MSGRVGDLSPKQEELAKFRENQDVLPALPNPDDYFLRLWRARSFDLQLSEAMLRKHV	60	-:- SUBUNIT: Monomer (By similarity).
Qy	40	---KRTITTSIAWQPPIQQLSGNCIGYDGPWYDGPDAKGILFSASKQL	95	-:- SUBCELLULAR LOCATION: Cycloplasmic in absence of alpha-tocopherol, and nuclear in presence of alpha-tocopherol (By similarity).
Db	61	EPRKQDKIDKIKISWPPIPVIQQLSGNCIGYDGPWYDGPDAKGILFSASKQL	120	-:- SIMILARITY: Contains 1 CRAL-Trio domain.
Qy	96	LRTKMRCECELLQECAHDTKLGRKVETITLYDCEGLGLKHLWKDAVEAYGEFLCMEE	155	-:- SIMILARITY: Contains 1 GOLD domain.
Db	121	LRTKMRCECELLQECAHDTKLGRKVETITLYDCEGLGLKHLWKDAVEAYGEFLCMEE	180	-- This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
Qy	156	NYPETLKLRLVYKAPKLEPVAVNLKIPFSELDTRKKIMVLGANVKEVLRHISPDQVPE	215	-- CC use as long as its content is in no way modified and this statement is not removed.
Db	181	NYPETLKLRLVYKAPKLEPVAVNLKIPFSELDTRKKIMVLGANVKEVLRHISPDQVPE	240	-- CC
DR		EMBL: BC005759; AAH05759_1; - ; mRNA.		-- CC
SMR		Q99J08; 1-396.		-- CC
DR		DR Ensembl; ENSMUSG0000003585; Mus musculus.		-- CC
MGI		MGI_1915055; Sec14_12.		-- CC
GO		GO_0005737; C:cytoplasm; ISS.		-- CC
GO		GO_0005634; C:nucleus; ISS.		-- CC
GO		GO_0005543; F:phospholipid binding; ISS.		-- CC
GO		GO_0008320; F:protein carrier activity; ISS.		-- CC
GO		GO_0016563; F:vitamin E binding; ISS.		-- CC
GO		GO_0008431; F:transcriptional activator activity; ISS.		-- CC
DR		DR GO_0045893; P:positive regulation of transcription, DNA-d.		-- CC
DR		DR GO_0045540; P:regulation of cholesterol biosynthesis; ISS.		-- CC
DR		DR InterPro; IPR001071; CRAL_b6 toc tran.		-- CC
DR		DR InterPro; IPR001251; CRAL_b6 TRIO_C.		-- CC
DR		DR InterPro; IPR008273; CRAL_b6 TRIO_C.		-- CC
DR		DR InterPro; IPR00348; Emp24_gp25L_p24.		-- CC
DR		DR InterPro; IPR009038; GOLD.		-- CC
Pfam		Pfam; PF00650; CRAL_TRIO; 1.		-- CC
Pfam		Pfam; PF01105; EMP24_gp25L; 1.		-- CC
PRINTS		PRINTS; PRO0180; SEC14_1.		-- CC
SMART		SMART; SM00116; SEC14_1.		-- CC
PROSITE		PROSITE; PS50191; CRAL_TRIO; 1.		-- CC
PROSITE		PROSITE; PS50866; GOLD; 1.		-- CC
KW		KW Activator; Lipid-binding; Nuclear protein; Transcription;		-- CC
FT DOMAIN		FT DOMAIN 76 249 CRAL_TRIO.		-- CC
FT DOMAIN		FT DOMAIN 275 383 GOLD.		-- CC
SEQUENCE		SEQUENCE 403 AA; 46300 MW; 420E0BABA004841 CRC64;		-- CC
Query		Query Match 85.5%; Score 1724.5; DB 1; Length 403;		-- CC
Best		Best Local Similarity 80.3%; Pred. No. 6.8e-132;		-- CC
Local		Local Matches 27; Mismatches 25; Indels 25; Gaps 2;		-- CC
Match		Match 326; Conservative 27; Mismatches 25; Indels 25; Gaps 2;		-- CC
Matches		Matches 326; Conservative 27; Mismatches 25; Indels 25; Gaps 2;		-- CC
Qy		1 MSGRVGDLSPROKELAK-----PEASTCRSRRRPCGSMWSSES-----39		-- CC
Db		1 MSGRVGDLSPROKELAKFRENQDVLPFLNPDDFLLLWRARSPLQKSEAMLRKHV 60		-- CC
Qy		40 -----KRLTTSIAWQPPIQQLSGNCIGYDGPWYDGPDAKGILFSASKQL 95		-- CC
Db		61 EPRKQDKIDKIKISWPPIPVIQQLSGNCIGYDGPWYDGPDAKGILFSASKQL 120		-- CC
Qy		96 LRTKMRCECELLQECAHDTKLGRKVETITLYDCEGLGLKHLWKDAVEAYGEFLCMEE 155		-- CC
Db		121 LRTKMRCECELLQECQTTKLGRKVETITLYDCEGLGLKHLWKDAVEAYGEFLCMEE 180		-- CC
Qy		156 NYPETLKLRLVYKAPKLEPVAVNLKIPFSELDTRKKIMVLGANVKEVLRHISPDQVPE 215		-- CC
Db		181 NYPETLKLRLVYKAPKLEPVAVNLKIPFSELDTRKKIMVLGANVKEVLRHISPDQVPE 240		-- CC
Qy		216 YGGTMPTDPGNPKCKSKINYGDDIPIKYYDQVKKQYEHVLSQGSSSHQVEYELFPG 275		-- CC
Db		241 YGGTMPTDPGNPKCKSKINYGDDIPIKYYDQVKKQYEHVLSQGSSSHQVEYELFPG 300		-- CC
Qy		276 CVLRWQMSGADGIVGFGIPLTKMGGRQRASEMTTEVLPNQYNSLYPEDGTLTCSDPGI 335		-- CC
Db		301 CVLRWQMSSEGSDGFSEIPLTKMGGRQRASEMTTEVLPNQYNSLYPEDGTLTCSDPGI 360		-- CC
Qy		336 YVLFNDNTYSPIHAKCYNFTVBLPLDPKASEEKMQLGAGTPK 378		-- CC
Db		361 YVLFNDNTYSPIHAKCYNFTVBLPLDPKASEEKMQLGAGTPK 403		-- CC

RC	STRAIN=Wistar; TISSUE=Liver;
RX	PubMed=11226224; DOI=10.1073/pnas.041620398;
RA	Shibata N., Arita M., Misaki Y., Dohmae N., Ono T., Inoue K., Arai H.;
RA	"Supernatant protein factor, which stimulates the conversion of squalene to lanosterol, is a cytosolic squalene transfer protein and enhances cholesterol biosynthesis.", Proc. Natl. Acad. Sci. U.S.A. 98:2244-2249 (2001).
RT	"Supernatant protein factor, which stimulates the conversion of squalene to lanosterol, is a cytosolic squalene transfer protein and enhances cholesterol biosynthesis.", Proc. Natl. Acad. Sci. U.S.A. 98:2244-2249 (2001).
AC	10-MAY-2005 (T-REMBLrel. 30, Created)
DT	10-MAY-2005 (T-REMBLrel. 30, Last sequence update)
DT	10-MAY-2005 (T-REMBLrel. 30, Last annotation update)
DE	SEC14-like 2 (S. cereviciae).
GN	Name=Sec14_12; ORFNames=RP23-81P12.5-006;
OS	Mus musculus (Mouse); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID	10090;
[1]	NCBI_TaxID=10090;
RN	
NUCLEOTIDE SEQUENCE.	
RA	Matthews L.; Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL	Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR	EMLB; AL807395; CAI205050.1; -; Genomic DNA.
SEQUENCE	403 AA; 46300 MW; 4208BAFB3004841 CRC64;
Query Match	85.5%; Score 1724.5; DB 2; Length 403;
Best Local Similarity	80.9%; Pred. No. 6.8e-132;
Matches	326; Conservative 27; Mismatches 25; Indels 25; Gaps 2;
db	1 MSGRVGDLSPROKEALAK-----PEASTCRSRPCGSMSSES----- 39
Qy	1 MSGRVGDLSPROKEALAK-----PEASTCRSRPCGSMSSES----- 39
db	1 MSGRVGDLSPROKEALAK-----PEASTCRSRPCGSMSSES----- 39
Qy	40 ---KRTLTTSLAWQPPEVQQYLSSGMCGYLDGCPWYDITGPDKAGLIFSSASKQL 95
db	61 EPRKQKDIDKIISSWQDQCLQQCTQQTKLKGKIEITMITYDCSIGHLGRCYDQGSPQDQL 120
Qy	96 LRTKMRBELLQOCBQHPTKGRKVETITLYDCIGLGLKHLWKPAVEYGEFLMEE 155
db	121 LRTKMRBELLQOCBQHPTKGRKVETITLYDCIGLGLKHLWKPAVEYGEFLMEE 180
Qy	156 NYPETKLRLFVYKAFLKPVAVNLKPLFSEDRTRKIMVLGANYKEYLVKHISPDQVPE 215
db	181 NYPETKLRLFVYKAFLKPVAVNLKPLFSEDRTRKIMVLGANYKEYLVKHISPDQVPE 240
Qy	216 YGGTMMTDGPNPKCKSKNKGDDIPRKYVYRDQKQOYEHSYQIISRGSSHOVEYLIFPG 275
db	241 YGGTMMTDGPNPKCKSKNKGDDIPRKYVYRDQKQOYEHTYQVSRSQSHQVEYLIFPG 300
Qy	276 CVLRWFQNSDADVGFGFLKTKMGERAGENTEVLNQRNISHLNFEDGTLTCSPGI 335
db	301 CVLRWFQNSDADVGFGFLKTKMGERAGENTEVLNQRNISHLNFEDGTLTCSPGI 360
Qy	336 YVLRFDNTYSFIHAKYNTFTVEVLLPDKASEEKMKGAGTPK 378
db	361 YVLRFDNTYSFIHAKYNSFTVEVLLPDKASEEKMKGAGTPK 403
RESULT 6	
ID	S14L2 RAT
ID	S14L2 RAT STANDARD
PRT	403 AA.
AC	Q99MS0;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	10-MAY-2005 (Rel. 47, Last annotation update)
DE	SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP) (Supernatant protein factor) (SPE) (Squalene transfer protein).
DE	Name=Sec14_12;
OS	Rattus norvegicus (Rat);
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID	10116;
RN	
NUCLEOTIDE SEQUENCE AND PROTEIN SEQUENCE OF 19-51 AND 231-252.	

- FUNCTION: carrier protein. Binds to some hydrophobic molecules and promotes their transfer between the different cellular sites.
- Binds with high affinity to alpha-tocopherol. Also binds with a weaker affinity to other tocopherols and to tocotrienols. May have a transcriptional activatory activity via its association with alpha-tocopherol. Probably recognizes and binds some squalene structure, suggesting that it may regulate cholesterol biosynthesis by increasing the transfer of squalene to a metabolic active pool in the cell (By similarity).
- SUBUNIT: Monomer.
- SUBCELLULAR LOCATION: Cytoplasmic in absence of alpha-tocopherol, and nuclear in presence of alpha-tocopherol (By similarity).
- SIMILARITY: Contains 1 CRAL-TRIO domain.
- SIMILARITY: Contains 1 GOLD domain.

216 VCGTMTDOPGNCPKCSKSTNYGGDPKCKYVDRDOKYOEHVOISRGSSHOVEYLFPG 275
Qy 180 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 NYPTELKRULFTIVAKPLFVPAVNLUVKPFLSEDTRKIQVIGANWKEVILKYISDQLPVE 240
Cv

Db	241	YGGTIDPDPGNPKCSKESKINNGGDIKKYYRDQVQQYERSVQISRGSSHOVEYRLFPG	300
Qy	276	CYLRQFMSDGAIVFGIFIKTKMGERQRAGEMTEYLPNORYNSHLVPEDGTLTCSDPGI	335
Db	301	CYLRQFMSDGSDFGIFIKTKMGERQRAGEMTEYLPSQYSAHHLVPEDSLLTCSDPGI	360
Qy	336	YVLRFDTNTYSPFHAKKUNFTYEVLLPD	362
Db	361	YVLRFDTNTYSPFHAKKVSFTYDVLLPD	387
RESULT 9			
	Q6PDG1_HUMAN	PRT;	392 AA.
	ID Q6PDG1_HUMAN PRELIMINARY;		
	AC Q6PDG1_		
	DT 05-JUL-2004 (TREMBLrel. 27, Created)		
	DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
	DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
	DE SEC14L2 protein.		
	GN Name=SEC14L2;		
	OS Homo sapiens (Human).		
	OC Mammalia; Metazoa; Chordata; Craniata; Vertebrates; Eureleostomi; Hominiidae;		
	OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;		
	OC Homo.		
	RN [1]	NCBI_TaxID=9606;	
	RP NUCLEOTIDE SEQUENCE.		
	RC TISSUE=Brain;		
	RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
	RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
	RA Klausner R.D., Collins F.S., Wagner L., Schuler G.D.,		
	RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
	RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
	RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
	RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,		
	RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
	RA Hara S.S., Loqueline N.A., Peters G.J., Abramson R.D., Mullahay S.J.,		
	RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
	RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
	RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
	RA Fahy J., Helton E., Keretsev M., Madan A., Rodriguez S., Sanchez A.,		
	RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
	RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
	RA Rodriguez A.C., Grimes J., Schmutz J., Myers R.M.,		
	RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,		
	RA Scheiner A., Schein J.E., Jones S.J.M., Marrs M.A.,		
	RT "Generation and initial analysis of more than 15,000 full-length human		
	RT and mouse cDNA sequences";		
	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
	RN [2]	NUCLEOTIDE SEQUENCE.	
	RP TISSUE=Brain;		
	RC Director MGC Project;		
	RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.		
	DR EMBL; BC058915; AAH56915.1; - mRNA.		
	DR SMR; Q6PDG61_1-360		
	DR GO; GO:0005622; C:intracellular; IEA.		
	DR GO; GO:0016020; C:membrane; IEA.		
	DR GO; GO:0009289; F:lipid binding; IEA.		
	DR GO; GO:0008320; F:protein carrier activity; IEA.		
	DR GO; GO:0019841; F:retinol binding; IEA.		
	DR GO; GO:0005215; F:transporter activity; IEA.		
	DR GO; GO:0006646; F:intracellular protein transport; IEA.		
	DR GO; GO:0006810; P:transport; IEA.		
	DR GO; GO:0007501; P:visual perception; IEA.		
	DR InterPro; IPR001251; CRAL_TRIO_C.		
	DR InterPro; IPR008273; CRAL_TRIO_N.		
	DR InterPro; IPR000348; Emp24_sp25L_P24.		
	DR InterPro; IPR001071; RetBind/toCTrans.		
	PFam; PF00650; CRAL_TRIO_1.		
	PFam; PF03785; CRAL_TRIO_N_1.		
	PFam; PF01105; Emp24_gp25L_1.		

DR PRINTS; PRO0180; CRETINALDHPB.	DR PRINTS; PR00180; CRETINALDHPB.
DR SMART; SM00516; SEC14; 1.	DR SMART; SM00516; SEC14; 1.
DR PROSITE; PS0191; CRAL_TRIO; 1.	DR PROSITE; PS0191; CRAL_TRIO; 1.
SEQ SEQUENCE; 392 AA; 44747 MW; 11A813345968FESA CRC64;	KW hypothetical protein.
	SEQUENCE 392 AA; 44768 MW; BDC2D956378ABEES CRC64;
Query Match 79.6%; Score 1606.5; DB 2; Length 392;	Query Match 78.3%; Score 1580.5; DB 2; Length 392;
Best Local Similarity 85.6%; Pred. No. 2, 7e-122;	Best Local Similarity 83.9%; Pred. No. 3, 6e-120;
Matches 308; Conservative 9; Mismatches 18; Indels 25; Gaps 2;	Matches 302; Conservative 13; Mismatches 20; Indels 25; Gaps 2;
Qy 1 MSGRVGDDSPROKEALAK-----PEASTCRSRPCGSMSSES---- 39	Qy 1 MSGRVGDDSPROKEALAK-----PEASTCRSRPCGSMSSES---- 39
Db 1 MSGRVGDDSPROKEALAKFRENQDVLPALPNPDDYTLRNLARSDLQKSEAMLRKHV 60	Db 1 MSGRVGDDSPROKEALAKFRENQDVLPALPNPDDYTLRNLARSDLQKSEAMLRKHV 60
Qy 40 ---KRTITTSLAWQPPVIOQYLGGCGYDGLGCPWYDILGPKDAGKLFSASKQL 95	Qy 40 ---KRTITTSLAWQPPVIOQYLGGCGYDGLGCPWYDILGPKDAGKLFSASKQL 95
Db 61 EFRKQKDIDNITISWPQPPVIOQYLGGCGYDGLGCPWYDILGPKDAGKLFSASKQL 120	Db 61 EFRKQKDIDNITISWPQPPVIOQYLGGCGYDGLGCPWYDILGPKDAGKLFSASKQL 120
Qy 96 LRTKMRRECELLQOCARTHTRKLGRKVETITIYDCBGLKHLWKPAVEAGEFLCMFEE 155	Qy 96 LRTKMRRECELLQOCARTHTRKLGRKVETITIYDCBGLKHLWKPAVEAGEFLCMFEE 155
Db 121 LRTKMRRECELLQOCARTHTRKLGRKVETITIYDCBGLKHLWKPAVEAGEFLCMFEE 180	Db 121 LRTKMRRECELLQOCARTHTRKLGRKVETITIYDCBGLKHLWKPAVEAGEFLCMFEE 180
Qy 156 NYPETLKLRFVVKAPKLFVPAVNLKPFLSEDTRKKIMVLGANYKEVLLKHSIPDQYVPE 215	Qy 156 NYPETLKLRFVVKAPKLFVPAVNLKPFLSEDTRKKIMVLGANYKEVLLKHSIPDQYVPE 215
Db 181 NYPETLKLRFVVKAPKLFVPAVNLKPFLSEDTRKKIMVLGANYKEVLLKHSIPDQYVPE 240	Db 181 NYPETLKLRFVVKAPKLFVPAVNLKPFLSEDTRKKIMVLGANYKEVLLKHSIPDQYVPE 240
Qy 216 YGGTMTDPDGPNPKCKSKINYGGDIPIRKYVVDQVKQOEHSHQVBYETLFPG 275	Qy 216 YGGTMTDPDGPNPKCKSKINYGGDIPIRKYVVDQVKQOEHSHQVBYETLFPG 275
Db 241 YGGTMTDPDGPNPKCKSKINYGGDIPIRKYVVDQVKQOEHSHQVBYETLFPG 300	Db 241 YGGTMTDPDGPNPKCKSKINYGGDIPIRKYVVDQVKQOEHSHQVBYETLFPG 300
Qy 276 CVLRWQFNSDGAIVGFGFLKTGMGRQRAGEMTEVLPNQRYNSHLVPEDGTLTCDPGI 335	Qy 276 CVLRWQFMSDGAIVGFGFLKTGMGRQRAGEMTEVLPNQRYNSHLVPEDGTLTCDPGI 335
Db 301 CVLRWQFNSDGAIVGFGFLKTGMGRQRAGEMTEVLPNQRYNSHLVPEDGTLTCDPGI 360	Db 301 CVLRWQFMSDGAIVGFGFLKTGMGRQRAGEMTEVLPNQRYNSHLVPEDGTLTCDPGI 360
RESULT 10	RESULT 11
Q3REK6_PONPY PONPY PRELIMINARY; PRT; 392 AA.	S14L3_HUMAN STANDARD; PRT; 400 AA.
AC Q3REK6_PONPY	ID S14L3_HUMAN
DT 01-FEB-2005 (TREMBLrel. 29 Created)	ID Q9UDX7
DT 01-FEB-2005 (TREMBLrel. 29 Last sequence update)	DT DT 10-OCT-2003 (Rel. 42, Created)
DT 01-FEB-2005 (TREMBLrel. 29 Last annotation update)	DT DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein DKFZp459B2422.	DE DE SEC14-like protein 3 (Tocopherol-associated protein 2).
GN Name=DKFZp459B2422;	GN GN Name=SEC14L3; Synonyms=TAP2;
OS Pongo pygmaeus (Orangutan)	OS Homo sapiens (Human)
CC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Pongo	OC Homo.
NCBI_TaxID=9600;	OC NCBITaxonID=9600;
RN [1]	RN [1]
RP NUCLEOTIDE SEQUENCE.	RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC TISSUE-Cortex;	RX MEDLINE=20057165; PubMed=10591208; DOI=10.1093/molbev/msb0031;
RG The German cDNA Consortium;	RX MEDLINE=22642877; PubMed=12757856; DOI=10.1016/S0891-5849(03)00173-4;
RA Ottenweller B., Obermaier B., Deutschenbaur S., Schaiapp A.,	RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.,	RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babage O.K.,
RA Submitted '(NOV-2004)' to the EMBL/GenBank/DBJ databases.	RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
DR SMBL; OR87519; CAH89801.1; -; mRNA.	RA Bird C.P., Blakley S.E., Bridgeman A.M., Buck D., Burgess J.,
DR Q3REK6_1-356;	RA Burill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,
DR GO; GO:0005622; C:intracellular; IEA.	RA Clegg S.M., Cobley V.E., Cole C.G., Connor R.,
DR GO; GO:0016020; C:membrane; IEA.	RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
DR GO; GO:0008289; F:lipid binding; IEA.	RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
DR GO; GO:0008340; F:protein carrier activity; IEA.	RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
DR GO; GO:0019841; F:retinol binding; IEA.	RA Gilbert J.G.R., Gowd M.B., Griffiths M.N.D., Hall C.,
DR GO; GO:0005215; F:transporter activity; IEA.	RA Hall R.B., Hall-Taylor G., Heathcott R.W., Ho S., Holmes S.,
DR InterPro; IPR008273; CRAL_TRIO_N.	RA Hunt S.E., Jones M.C., Kershaw J., Kimber A.M., King A.,
DR InterPro; IPR000848; Emp24_gp25L.	RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
DR InterPro; IPR0010101; RetBind/toctrans.	RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
DR Pfam; PF03765; CRAL_TRIO_N; 1.	RA
DR Pfam; PF01105; EMP24_gp25L; 1.	RA

RX	MEDLINE=39277573; PubMed=10350070; DOI=10.1016/S0014-5793(99)00470-6;	Db	361 YVLRFDNTYSFVHAKKVSTVVEVLLPDEGMQKYDEEL--TP 399
RA	Merkulova M.I., Andreeva S.G., Shuvayeva T.M., Novoselov S.V., Pesheva I.V., Bystrrova M.F., Novoselov V.I., Resenko E.E., Lipkin V.M.; "A novel 45 kDa secretory protein from rat olfactory epithelium: primary structure and localization.", RSL Lett. 450:1126-130 (1999).	RESULT 15	RESULT 15
RT		ID Q5SQ27_MOUSE PRELIMINARY; PRT; 401 AA.	ID Q5SQ27_MOUSE PRELIMINARY; PRT; 401 AA.
RL		AC Q5SQ27_	AC Q5SQ27_
CC	-!- FUNCTION: Probable hydrophobic ligand-binding protein; may play a role in the transport of hydrophobic ligands like tocopherol, squalene and phospholipids.	DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)	DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
CC	-!- TISSUE_SPECIFICITY: Detected in a layer of supportive cells in olfactory epithelium, in the apical region of the trachea and in the surface layer of ciliated bronchial epithelium in the lung.	DE Novel protein, ortholog of 'human and rat SC14-like 3 (S. cerevisiae)' SBC14L3.	DE Novel protein, ortholog of 'human and rat SC14-like 3 (S. cerevisiae)' SBC14L3.
CC	-!- PRM: The N-terminus seems to be blocked.	GN Name=OrfMUSP00000005238; ORFNames=RP23-81P12.8-001;	GN Name=OrfMUSP00000005238; ORFNames=RP23-81P12.8-001;
CC	-!- SIMILARITY: Contains 1 CRAL-TRIO domain.	OS Mus musculus (Mouse)	OS Mus musculus (Mouse)
CC	-!- SIMILARITY: Contains 1 GOLD domain.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murinae; Muridae; Mus.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murinae; Muridae; Mus.
CC		NCBI_TaxID=1090;	NCBI_TaxID=1090;
CC		RN [1.]	RN [1.]
CC		RP Nucleotide Sequence.	RP Nucleotide Sequence.
CC		RA Matthews L.	RA Submitted (PEB-2005) to the EMBL/GenBank/DBJ databases.
CC		RL DR EMBL; AL807395; CAI26047.1; -; Genomic_DNA.	RL DR EMBL; AL807395; CAI26047.1; -; Genomic_DNA.
CC		DR SNR; Q5SQ27; 1-38.	DR SNR; Q5SQ27; 1-38.
CC		DR GO; GO:0005622; C: intracellular; IEA.	DR GO; GO:0005622; C: intracellular; IEA.
CC		DR GO; GO:0016040; C: membrane; IEA.	DR GO; GO:0016040; C: membrane; IEA.
CC		DR GO; GO:0008300; F: transporter carrier activity; IEA.	DR GO; GO:0008300; F: transporter carrier activity; IEA.
CC		DR GO; GO:0005215; F: transporter activity; IEA.	DR GO; GO:0005215; F: transporter activity; IEA.
CC		DR GO; GO:0068846; F: intracellular protein transport; IEA.	DR GO; GO:0068846; F: intracellular protein transport; IEA.
CC		DR InterPro; IPR001251; CRAL_TRIO_C.	DR InterPro; IPR001251; CRAL_TRIO_C.
CC		DR InterPro; IPR008273; CRAL_TRIO_N.	DR InterPro; IPR008273; CRAL_TRIO_N.
CC		DR InterPro; IPR000348; Emp24_gp25L_p24.	DR InterPro; IPR000348; Emp24_gp25L_p24.
CC		DR InterPro; IPR009038; GOLD.	DR InterPro; IPR009038; GOLD.
CC		DR InterPro; IPR001011; RetBind/toctrans.	DR InterPro; IPR001011; RetBind/toctrans.
CC		DR PFAM; PF00650; CRAL_TRIO_1.	DR PFAM; PF00650; CRAL_TRIO_1.
CC		DR PFAM; PF03765; CRAL_TRIO_N; 1.	DR PFAM; PF03765; CRAL_TRIO_N; 1.
CC		DR PFAM; PF01105; EMP24_gp25L; 1.	DR PFAM; PF01105; EMP24_gp25L; 1.
CC		DR PFANTS; PR00580; CRETINALDHPB.	DR PFANTS; PR00580; CRETINALDHPB.
CC		DR SMART; SMO00516; SEC14; 1.	DR SMART; SMO00516; SEC14; 1.
CC		DR PROSITE; PS50191; CRAL_TRIO_1.	DR PROSITE; PS50191; CRAL_TRIO_1.
CC		DR PROSITE; PS50866; GOLD; 1.	DR PROSITE; PS50866; GOLD; 1.
CC		DR PROSITE; PS55191; CRAL_TRIO_1.	DR PROSITE; PS55191; CRAL_TRIO_1.
CC		SQ SEQUENCE 401 AA; 46027 MW; 548A72DDA9B4FC26 CRC64;	SQ SEQUENCE 401 AA; 46027 MW; 704A92A72F82FB57 CRC64;
CC		Query Match Score 1413; DB 1; Length 400;	Query Match Score 1408.5; DB 2; Length 401;
CC		Best Local Similarity 65.9%; Pred. No. 1.6e-106;	Best Local Similarity 66.0%; Pred. No. 3.8e-106;
CC		Matches 52; Mismatches 57; Indels 28; Gaps 4;	Matches 266; Conservative 51; Mismatches 57; Indels 29; Gaps 5;
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QY	1 MSGRVGDLSPROKEALK-----PEASTCRSRPCCGSMSSES-----39	Db 1 MSGRVGDLSPROKEALK-----PEASTCRSRPCCGSMSSES-----39	Db 1 MSGRVGDLSPROKEALK-----PEASTCRSRPCCGSMSSES-----39
Db	40 -KRTLTTS--LAQWOPPEVIOQYLSECGMCGYDLDGCPWYDITGPKDAKGLFSASKQDL 95	Qy 40 --KRTLTTS--LAQWOPPEVIOQYLSECGMCGYDLDGCPWYDITGPKDAKGLFSASKQDL 95	Qy 40 --KRTLTTS--LAQWOPPEVIOQYLSECGMCGYDLDGCPWYDITGPKDAKGLFSASKQDL 95
Db	61 EFRKTMDIDHLDWQPPEVIOQYKMPGCLGQYDRGCPWYDITGPKGLFSVTQKDL 120	Db 61 EFRKTMDIDHLDWQPPEVIOQYKMPGCLGQYDRGCPWYDITGPKGLFSVTQKDL 120	Db 61 EFRKTMDIDHLDWQPPEVIOQYKMPGCLGQYDRGCPWYDITGPKGLFSVTQKDL 120
QY	96 LRTKMRCECELLQECAHQRTKLGRKVETITIYDCEGLGLKHLWNPVAEAYGEFLCMFEE 155	Qy 96 LRTKMRCECELLQECAHQRTKLGRKVETITIYDCEGLGLKHLWNPVAEAYGEFLCMFEE 155	Qy 96 LRTKMRCECELLQECAHQRTKLGRKVETITIYDCEGLGLKHLWNPVAEAYGEFLCMFEE 155
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Db	181 NYPETLKRFLIVKAPKLFPVAYNLKIPFLESDTRKKIMVLANGYKEVLKXKHISPROVPE 240	Db 181 NYPETLKRFLIVKAPKLFPVAYNLKIPFLESDTRKKIMVLANGYKEVLKXKHISPROVPE 240	Db 181 NYPETLKRFLIVKAPKLFPVAYNLKIPFLESDTRKKIMVLANGYKEVLKXKHISPROVPE 240
QY	216 YGGTMWPDGPNPKCKSKINNGDIPRKYVYRDQVKOYERSVQISRGSSHOVQEYBILFP 275	Qy 216 YGGTMWPDGPNPKCKSKINNGDIPRKYVYRDQVKOYERSVQISRGSSHOVQEYBILFP 275	Qy 216 YGGTMWPDGPNPKCKSKINNGDIPRKYVYRDQVKOYERSVQISRGSSHOVQEYBILFP 275
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QY	276 CVLRWQFMSDGAQDVGFLFLKTMGERQRAGEMTEVLPNQRYNSHLVPEDGTLTCSDPG 335	Qy 276 CVLRWQFMSDGAQDVGFLFLKTMGERQRAGEMTEVLPNQRYNSHLVPEDGTLTCSDPG 335	Qy 276 CVLRWQFMSDGAQDVGFLFLKTMGERQRAGEMTEVLPNQRYNSHLVPEDGTLTCSDPG 335
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Db 361 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
VYVLRFDNTSYHAKKSFTVEVLLPDEGMOKYDBEL--TP 400

Search completed: May 2, 2006, 18:38:13
Job time : 235 secs

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GenCore version 5.1.7

protein search, using sw model

on: May 2, 2006, 18:38:32 ; search time 47 Seconds
 (without alignments)
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scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 572060 seqs, 82675679 residues

total number of hits satisfying chosen parameters: 572060

minimum DB seq length: 0
 maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

database : Issued Patents AA:
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 3: /cgcn2_6_ptodata/1/iaa/H COMB.pep:/*
 4: /cgcn2_6_ptodata/1/iaa/BCTUS COMB.pep:/*
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 6: /cgcn2_6_ptodata/1/iaa/RE.backfiled.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12772	63.0	391	2 US-10-104-047-2798	Sequence 2798, AP
2	1118	55.4	360	2 US-10-104-047-3609	Sequence 3609, AP
3	394	19.5	723	2 US-09-949-016-3810	Sequence 9810, AP
4	344.5	17.1	308	2 US-09-270-767-33202	Sequence 33202, A
5	344.5	17.1	308	2 US-09-270-767-38419	Sequence 48419, A
6	197	9.8	304	2 US-09-538-092-613	Sequence 613, App
7	181.5	9.0	293	2 US-09-248-796A-18524	Sequence 18524, A
8	181	9.0	278	2 US-08-557-614-2	Sequence 2, App1
9	181	9.0	278	2 US-08-557-614-23	Sequence 23, App1
10	144	7.1	330	2 US-09-270-767-33290	Sequence 43290, A
11	124	6.1	301	2 US-09-270-767-43653	Sequence 43653, A
12	115.5	5.7	341	2 US-09-244-005-61	Sequence 61, App1
13	114.5	5.7	136	2 US-09-270-767-32985	Sequence 32985, A
14	114.5	5.7	136	2 US-09-270-767-48202	Sequence 48202, A
15	111.5	5.6	342	2 US-09-244-005-62	Sequence 62, App1
16	111	5.5	316	2 US-09-270-767-43378	Sequence 43378, A
17	111	5.5	778	2 US-09-270-767-45008	Sequence 45008, A
18	110	5.5	317	2 US-09-349-016-5927	Sequence 5927, App1
19	110	5.5	344	2 US-09-949-016-9447	Sequence 9647, App1
20	110	5.5	343	2 US-09-507-765-30	Sequence 20, App1
21	110	5.5	433	2 US-09-307-765-31	Sequence 31, App1
22	109	5.4	274	2 US-09-270-767-32136	Sequence 32136, A
23	109	5.4	274	2 US-09-270-767-47353	Sequence 47353, A
24	109	5.4	823	2 US-09-370-767-42450	Sequence 42450, A
25	107	5.3	135	2 US-09-270-767-58728	Sequence 58728, A
26	107	5.3	342	2 US-09-270-767-60040	Sequence 60491, A
27	107	5.3	342	2 US-09-348-796A-15115	Sequence 15115, A

ALIGNMENTS

RESULT 1
 US-10-104-047-2798
 ; Sequence 2798, Application US/10104047
 ; Patent No. 6943241
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIXX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: NO. 6943241el full length cDNA
 ; FILE REFERENCE: HI-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104, 047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2798
 ; LENGTH: 391
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-104-047-2798

Query Match 60.0%; Score 1272; DB 2; Length 391;
 Best Local Similarity 62.0%; Pred. No. 3.1e-138;
 Matches 232; Conservative 58; Mismatches 68; Indels 16; Gaps 20

Qy 20 EASTCRSRRPCSGS-----MWSSE--SKRTLTTSIWAQPPEVYQYTLGGM 63
 Db 14 ETLTCRNPKTCSEGPKSPQPTSCPHALRHWMEFKQDLDNIVTWQPPEVYQLIDSGLL 73

Qy 64 CGYLDGCPWYD1GPKDAGKLFSASKDQLRTKMRCECAHOTTKLGRKVET 12
 Db 74 CGYDVEGCPVYFNITLGSLDQPKGLLSASKDQMIRKVCVELQHCELOVQKLGRKIE 13

Qy 124 ITTYDCEGUGLKHLWKPAVEAYGEPCLMFPEENYPTLKLFLVYKPLFPVANLIKPF 18
 Db 134 ALLFDEMEGLSLKHLWKPAVEVYQQFESILEANYPTLKNLIVTRAPKLFPVAFNLVKSF 19

Qy 184 LSEDTKKKIMVLYKANVKEVLLKHISPDQPVYEGGTMTDPGNPKCKSKKINYGDLPRKY 24
 Db 194 MSEETRKVILGDWKQELTKFISPDQLPTEFGTMTPDGPNPKCLTKLNKGYPKSY 25

Qy 244 YRDQVQQYEHSVQ1TSRGSSHSQVEYBILFFPGCVRWFQMSDADYGFGLFKTKNGERO 30
 Db 254 YLCEDQYLOVLEHTRSYGRGSLSQVENEILBLQFVAFKTRKGQBBQ 31

Qy 304 RAGEMTEVLVNPQRNQNSHLVLPEDGTLTCDPGIYVLRFDNTYSPITHAKKVNFTVEVILPDK 36
 Db 314 SAREMTEVLPSQRYNAMVMPEDGSLSITCLQagvYVLRFDNTYSRMVKLSVTVEVILPDK 37

Qy 364 ASEKMKQKLQACTP 377

Db 374 ASBETOSLAKMRP 387
 RESULT 2
 US-10-104-047-3609
 ; Sequence 3609 Application US/10104047
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. 694241ei full length cDNA
 ; FILE REFERENCE: H1-A105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIORITY NUMBER:
 ; PRIORITY FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 3609
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-104-047-3609

Query Match Score 19.5%; Score 394; DB 2; Length 723;
 Best Local Similarity 23.7%; Pred. No. 5.2e-36;
 Matches 111; Conservative 83; Mismatches 164; Indels 110; Gaps 14;

Qy 5 VGDLSPROKEBALAKPE---ASTCRSRP-----CSGMNSSE 38
 Db 256 LGDTPLQSCLIRLRQWLOETHKSKIPDEHLRFLARDNTIKAREIMCQLSLTRKQ 315

Qy 39 SKRLTTSLAWQPPEVIIQQYLSGGMCGYDLDGCPWYDIIGPKDAKGLLFSASKQDLRLRT 98
 Db 316 HQVDYLE-TWTPSQLQDYYAGEWHHHDGRPLYVRLRGQMDTKGLVTALEGEEALLRY 374

Qy 99 KMRCECLLQECAHTTGLRKVETITIYDCEGLGLKLHMKPAVEAYGEFLCMPPENYP 158
 Db 375 VLSINEGLRRCENTKVFRPISSWTCLVDELMRMRLWRPGTYKAHLRLIEVWANYP 434

Qy 159 ETLKRLFVYKAPLFPAVNLIKPLSEDTRKKTMVLGANYKE--VLLRHISPDQVVPVE 215
 Db 435 ETLGRLLILRAPRPFVPLWLTSPIDDDNTRKFLIYAGNDYQGPGLLDDYDKEIIPDF 494

Qy 216 YGGTMTDPDGNCPKCKSINKYGGDIPRKYYRDQVVKQYEH-----SVQISRGQS 263
 Db 495 LSG-----ECMCEVPEGGLVPSLY--RTEAELNEIDLKWLWETIYQSAVFKGA 542

Qy 264 SHQEVEYEILFPGCVYLWQFMSDGAvgFGIFLKTMGE--QRAGEMTEVLPNQYNSH 320
 Db 543 PHEILLQIVDASSVITWDFDVCKGDPIVFNHYHSKRSPOPQPKKDSLGAAHSITSPGGN-NVQ 601

Qy 321 LVPE-----DTGLTCD-----PGIYVL-----RFD 341
 Db 602 LIDKWWQLGRDYSMSVESPICKEGBSVQGSHTVRPGFYILOWKPHSMPCAASSIPLRVD 661

Qy 342 NTYSFI----HAKCNFTVEVLLPD-----KASEEKMKGKAGT 376
 Db 662 DVLASLQVSQSHHKCKWVMYTEVIGSDFRGSMTSLESQSGFSQLSMAT 709

RESULT 4
 US-09-270-767-33202
 ; Sequence 33202, Application US/09270767
 ; PRIORITY NUMBER: 6703-91
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270/767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 33202
 ; LENGTH: 308
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid

Query Match Score 17.1%; Score 344.5; DB 2; Length 308;
 Best Local Similarity 26.8%; Pred. No. 6.8e-31;
 Matches 91; Conservative 59; Mismatches 115; Indels 75; Gaps 8;

Qy 54 VIQQYLSGGMCGYDLDGCPWYDIIGPKDAKGLLFSASKQDLRLRTMRECBLLQCAHQ 113
 Db 2 VVVFEPGGWTHLDKDRPYVILRGMDYKGLKSLGMDLRLAHICREGIQKINES 61

Qy 114 TTKGURKVERITITIYDCEGLGLKLHMKPAVEAYGEFLCMPPENYP TLKRUVVKAPKLF 173
 Db 62 AERLEKPVLNWSSLVDEGLJSMRHLWRPGIKALLNTIETVERNYPETMGRLVVRAPRVF 121

Qy 174 PVAYNLKPKPLSEDTRKKTMVLG---ANYKEVLKHISPDQVVEYGGTMDTPDGNGPKCK 230
 Db 122 PIAWIVSAFIDEHTRSKFLFYPGDOAHMDGLAQDLEEVLPDFJLG-----PCK 172

RESULT 3
 US-09-949-016-9810
 ; Sequence 9810, Application US/0949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 287012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-9810

Qy 231 SKINYGGDIPRKYYVYRQVK-----SV 257
 : : : : : : : : : : : : : : : : : :
 Db 173 TMIHGGGLPKTLKMNNSLEDHDDETAELPTTAAQAQLVPGKRLSANQQDHRLNLYSV 232
 Qy 258 QISRGSSHHQEVEYLFPQCYLRFQMSGADYEGFIFLTKMGERQAGEMTEVLPNQRY 317
 : : : : : : : : : : : : : : : : : :
 Db 233 DLKAGFAELLRNEDPDKSFLTDMDVRNDLHFTLY-----RTVXELPEKND 280
 Qy 318 NSHLVPEDGTLCSDPGIVYLRFDTNTYSFHARKVNFTVE 357
 : : : : : : : : : : : : : : : : : :
 Db 281 SGRLV---LWICKD-----FVQGRPI-FSVE 302

RESULT 5
 US-09-270-767-48419
 Sequence 4419, Application US/09270767
 Patent No. 670491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 FILE REFERENCE: File Reference: 7226-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 48419
 LENGTH: 308
 TYPE: PRT
 ORGANISM: *Drosophila melanogaster*
 FEATURE:
 OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-48419

Query Match 17.1%; Score 344.5; DB 2; Length 308;
 Best Local Similarity 26.8%; Pred. No. 6.8e-31; Mismatches 59; Indels 75; Gaps 8;
 Matches 91; Conservative 59; Mismatches 115; Indels 75; Gaps 8;

Qy 54 VIOOYLSGAGMCYDLDGCPWYDINGPKDAKLGSASRQDLIIRTKMRECELLQECAHQ 113
 : : : : : : : : : : : : : : : : : :
 Db 2 VVBFHPGTHLDKGRPYILRLGHMDVKGKLSLGMGDLRLALICBQKINES 61
 Qy 114 TTKLGRKVETITIYDCESHLGLKHLMKPAVEAYGBFLCMFEENYPETKLRLKTFVYKAPLKF 173
 : : : : : : : : : : : : : : : : : :
 Db 62 AERLEKPVNLNSLVDLEGSLSMRHLWRPGTKALLNNIETVERNYPETNGRVLVRAPRF 121
 Qy 174 PAVNLKIEPKLSEDTTRKVMVLG---ANYKEVLKHKISPDQVYBEGGTMDDGNNPCK 230
 : : : : : : : : : : : : : : : : : :
 Db 122 PIAWTIVASAPIDENTRSKFLFYGPDCAMHKDGLAQLYDEEVPDFLGQ-----PCK 172
 Qy 231 SKINYGGDIPRKYYVYRQVK-----SV 257
 : : : : : : : : : : : : : : : : : :
 Db 173 TMIHGGGLPKTLKMNNSLEDHDDETAELPTTAAQAQLVPGKRLSANQQDHRLNLYSV 232
 Qy 258 QISRGSSHHQEVEYLFPQCYLRFQMSGADYEGFIFLTKMGERQAGEMTEVLPNQRY 317
 : : : : : : : : : : : : : : : : : :
 Db 233 DLKAGFAELLRNEDPDKSFLTDMDVRNDLHFTLY-----RTVXELPEKND 280

RESULT 6
 US-09-538-092-613
 Sequence 613, Application US/09538092
 Patent No. 6753314
 GENERAL INFORMATION:
 APPLICANT: Giot, Loic
 APPLICANT: Mansfield, Traci A.
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352
 PRIOR FILING DATE: 1994-04-01
 PRIOR APPLICATION NUMBER: 60/178,965
 PRIOR FILING DATE: 2000-02-01
 NUMBER OF SEQ ID NOS: 1387
 SOFTWARE: CurapatecSeFormatte Version 0.9
 SEQ ID NO: 613
 LENGTH: 304
 TYPE: PRT
 ORGANISM: *Saccharomyces cerevisiae*
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0) .(0)
 OTHER INFORMATION: Polypeptide Accession Number YMR079W
 US-09-38-092-613

Query Match 9.8%; Score 197; DB 2; Length 304;
 Best Local Similarity 30.6%; Pred. No. 8.4e-14;
 Matches 48; Conservative 36; Mismatches 63; Indels 10; Gaps 4;

Qy 67 DLDGCPWYDINGPKDAKLGSASRQDLIIRTKMRECELLQECAHQ 122
 : : : : : : : : : : : : : : : : : :
 Db 115 DRDGRPFYEEGLGKHLWPKPAVEAYGEFLCMPPEN-YPETKLRLKTFVYKAPLKFVYK 181
 Qy 123 TITIYDCEGLGKHLWPKPAVEAYGEFLCMPPEN-YPETKLRLKTFVYKAPLKFVYK 181
 : : : : : : : : : : : : : : : : : :
 Db 172 TSCIMDURGKISISAY-SVNSYVREASATTSQNYPERMGKFYIINAPFGSTAFRLFK 229
 Qy 182 PFLSSEDTRKKVIVLGANYKEVLKHKISPDQVYEGG 218
 : : : : : : : : : : : : : : : : : :
 Db 230 PFLDPVTVSFKIFLGSYQKELJKQIAPAENLPVKFGG 266

RESULT 7
 US-09-248-796A-18524
 Sequence 18524, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICATA
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196_132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO: 1524
 LENGTH: 293
 TYPE: PRT
 ORGANISM: *Candida albicans*
 US-09-248-796A-18524

Query Match 9.0%; Score 181.5; DB 2; Length 293;
 Best Local Similarity 30.6%; Pred. No. 5e-12; Mismatches 33; Indels 9; Gaps 4;

Qy 67 DLDGCPWYDINGPKDAKLGSASRQDLIIRTKMRECELLQECAHQ 122
 : : : : : : : : : : : : : : : : : :
 Db 115 DRDGRPVFEEGLGKHLWPKPAVEAYGEFLCMPPEN-YPETKLRLKTFVYKAPLKFVYK 171

Query Match 9.0%; Score 181.5; DB 2; Length 293;
 Best Local Similarity 30.6%; Pred. No. 5e-12; Mismatches 33; Indels 9; Gaps 4;

Qy 123 TITIYDCEGLGKHLWPKPAVEAYGEFLCMPPEN-YPETKLRLKTFVYKAPLKFVYK 122
 : : : : : : : : : : : : : : : : : :
 Db 172 TSCIMDURGKISISAY-VIGTREASKGQDYPERMGKFYIINAPFGSTAFRLFK 230

Query Match 9.0%; Score 181.5; DB 2; Length 293;
 Best Local Similarity 30.6%; Pred. No. 5e-12; Mismatches 33; Indels 9; Gaps 4;

Qy 183 FLSPEDTRKKVIVLGANYKEVLKHKISPDQVYEGG 222
 : : : : : : : : : : : : : : : : : :
 Db 231 SLDPVTVSFKIFLGSYQKELJKQIAPAENLPVKFGG-MSD 269

RESULT 8

US-08-557-614-2
 ; Sequence 2, Application US/08557614
 ; GENERAL INFORMATION:
 ; APPLICANT: Siddique, Teepu
 ; APPLICANT: Hentati, Afif
 ; APPLICANT: Deng, Han-Xiang
 ; TITLE OF INVENTION: Alpha-Tocopherol Transport Protein:
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 180 N. Stetson
 ; CITY: Chicago
 ; STATE: Illinois
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/557,614
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6268170chrup, Thomas E.
 ; REGISTRATION NUMBER: 33,268
 ; TELECOMMUNICATION INFORMATION:
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/557,614
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6268170chrup, Thomas E.
 ; REGISTRATION NUMBER: 33,268
 ; REFERENCE DOCKET NUMBER: NOR3446P00400US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 616-5400
 ; TELEFAX: (312) 616-5460
 ; INQUIRIES FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 278 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-557-614-2

Query Match 9.0% Score 181; DB 2; Length 278;
 Best Local Similarity 25.8%; Pred. No. 5.2e-12;
 Matches 56; Conservative 34; Mismatches 67; Indels 60; Gaps 7;

Qy 7 DLSPRKEALAKP-EASTCRSSRPGSMWSSESKRLTTSIAWQPPEVQQYLSGCMCG 65
 Db 86 DLHRSITGLKAGYHGVLRSRDP-TGS-----DVRVSLLTSELIVQEY-ETQRNGVKA--- 130

Qy 66 YDLDGCPWVYD1GPKDAKGILFSASKDILRTKRNCRECLLQCAHOTTKLGRKVETIT 125
 Db 131 -----DVRVSLLTSELIVQEY-ETQRNGVKA--- 156

Qy 126 IYDGCGLGKHLWIKRAVEVYCEFLCMEENYPECKRLFVVKAPKLFPVAYNLKPFLS 185
 Db 157 -IFDLCGWQ1SHAFQITPSVAKKIAAVTDSFLPLVYRGIHLNEPVIFHAFVSMIKPFLT 215

Qy 186 EDTRKIMVLAGNYKEVLLRKHSIDPVYEVGG 218
 Db 216 EKIGRHLHNNYKSLLQHF-PDILPEYGG 247

Db 131 -----DVFRVSLTSELIVQE-----VETQR 151

Qy 124 -ITIYDCEGLKHLWIKPAVEAYGEFLCMFEEENYPDTLKRFLVVKAPKLFPVANLIK 181
 Db 152 NGKAIKFLEGWQFSHAFQITPSVAKKIAAVLTDSPFLPKVGHLINEPVIFHAVESMK 211

Qy 182 PFLSDTRKKMIVLGANYKEVLLRKHSIDDVQPVYEVGG 218
 Db 212 PFLTEKIKERIHMGNNTKOSLQHF-PDILPEYGG 247

RESULT 9
 US-08-557-614-23
 ; Sequence 23, Application US/08557614
 ; GENERAL INFORMATION:
 ; APPLICANT: Siddique, Teepu
 ; APPLICANT: Hentati, Afif
 ; APPLICANT: Deng, Han-Xiang
 ; TITLE OF INVENTION: Alpha-Tocopherol Transport Protein:
 ; TITLE OF INVENTION: Compositions And Methods
 ; NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
 ; STREET: 180 N. Stetson
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/557,614
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6268170chrup, Thomas E.
 ; REGISTRATION NUMBER: 33,268
 ; REFERENCE/DOCKET NUMBER: NOR3446P00400US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 616-5400
 ; TELEFAX: (312) 616-5460
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 278 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-557-614-23

Query Match 9.0% Score 181; DB 2; Length 278;
 Best Local Similarity 25.8%; Pred. No. 5.2e-12;
 Matches 55; Conservative 36; Mismatches 70; Indels 52; Gaps 7;

Qy 7 DLSPRKEALAKP-EASTCRSSRPGSMWSSESKRLTTSIAWQPPEVQQYLSGCMCG 65
 Db 86 DLHRSITGLKAGYHGVLRSRDP-TGS-----DVRVSLLTSELIVQEY-ETQRNGVKA--- 130

Qy 66 YDLDGCPWVYD1GPKDAKGILFSASKDILRTKRNCRECLLQCAHOTTKLGRKVETIT 125
 Db 131 -----DVRVSLLTSELIVQEY-ETQRNGVKA--- 156

Qy 126 IYDGCGLGKHLWIKRAVEVYCEFLCMEENYPECKRLFVVKAPKLFPVAYNLKPFLS 185
 Db 157 -IFDLCGWQ1SHAFQITPSVAKKIAAVTDSFLPLVYRGIHLNEPVIFHAFVSMIKPFLT 215

Qy 186 EDTRKIMVLAGNYKEVLLRKHSIDPVYEVGG 218
 Db 216 EKIGRHLHNNYKSLLQHF-PDILPEYGG 247

RESULT 10
 US-09-270-767-43290
 ; Sequence 24, Application US/09270767
 ; Sequence 43290, Application US/09270767
 ; General Information:
 ; Patent No. 6703191
 ; General Information:
 ; Applicant: Homburger et al.
 ; Title of Invention: Nucleic acids and proteins of Drosophila melanogaster
 ; File Reference: 7326-094
 ; Current Application Number: US/09/270,767
 ; Current Filing Date: 1999-03-17
 ; Number of Seq ID Nos: 62517
 ; Seq ID No: 43290
 ; Length: 330
 ; Type: PRT
 ; Organism: Drosophila melanogaster
 ; US-09-270-767-43290

Query Match 7.1% Score 144; DB 2;
 Best Local Similarity 26.4%; Pred. No. 1.3e-07;

Matches 48; Conservative 27; Mismatches 53; Indels 54; Gaps 7;

Query 86 LIFSAASKQDILRTKRE-----CELILOQCAH-----

Db 121 LKVGAACENTIPSKLRLNPFEANTILNLIPORDGRRLLVLEAGRKWKPSQVPLVLDLFRGI 180

Query 113 QTTKLGRKVETIT----IYDEBGLGLHL--WKPAVEA----YGBFLCMFEENYPE 159

Db 181 QLTVLGSMEPFSQICCSVIIIMPEGLISHITQPTPFAFMALDYLIECIM---- 233

Query 160 TLKRLFLVYKAPLKPEPVAVNLIKEPKPFLSEDTRKTMVGLANYKEVLKHLISPDQVPVEYCGT 219

Query 234 RLKAVHVNNSYIFNMLFAVFKPFIREKURKRIFFHGKDYS-LISHFBAKALPPKYGGS 292

Query 220 MT 221

Db 293 At 294

RESULT 11

US-09-270-767-43653

Sequence 43653, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 43653

LENGTH: 301

TYPE: PRT

ORGANISM: *Drosophila melanogaster*

US-09-270-767-43653

Query Match 6.1%; Score 124; DB 2; Length 301;

Matches 41; Conservative 31; Mismatches 71; Indels 42; Gaps 6;

Query 84 KGLLESAASKQDLIR---TKRRECE---LLQBC-----A90T 114

Db 103 RGLLYEQVKERKEVKGSVINVLRKNCQKGRRVLYNCMVMHLA 162

Query 115 TKLGR--KVETITIYDCEGIGLKLHWKPAVEAYGGBFLCMFEENYPETKRLFTVKAPKLU 172

Db 163 AQLEEBTQRGVUCIMPEGLSMKQEAKALSPSKRKLTFIQEAMPLRAMEKEVHVKOPFFI 222

Query 173 FPPVATNLIKPKPFLSEDTRKTMVGLANYKEVLKHLISPDQVPVEYCGTMTDPGNPKCKSR 232

Db 223 FNMMWSLKFPKVQKLUNRMHFHGDSMKS-LQKFLDPSVLPANTKGTL-----PA 271

Query 233 INYGG 237

Db 272 IDYGG 276

RESULT 12

US 09-244-805-61

Sequence 61, Application US/09244805

Patent No. 6639660

GENERAL INFORMATION:

APPLICANT: Worley, Paul F.

APPLICANT: Lanahan, Anthony

APPLICANT: Goetz, Bernard

APPLICANT: Heimisch, Holger

APPLICANT: Kuner, Rohini

APPLICANT: Scheer, Sigrid

APPLICANT: Nikolich, Karoly

APPLICANT: Zhukowski, Eugene

TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 10496/004001
 ; CURRENT APPLICATION NUMBER: US/09/244, 805
 ; CURRENT FILING DATE: 199-02-05
 ; PRIOR APPLICATION NUMBER: 60/074, 518
 ; PRIOR FILING DATE: 1998-02-12
 ; PRIOR APPLICATION NUMBER: 60/074, 135
 ; PRIOR FILING DATE: 1998-02-06
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 61
 ; LENGTH: 341
 ; TYPE: PRT
 ; ORGANISM: *Rattus norvegicus*
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1) .. (341)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-244-805-61

Query Match 5.7%; Score 115.5; DB 2; Length 341;
 Best Local Similarity 22.5%; Pred. No. 0.0029;
 Matches 50; Conservative 36; Mismatches 85; Indels 51; Gaps 9;

Query 43 LTTSLAWOPEVITQQLSGGMCCSD-----LGCG---PWYDIDGPKDKGLLFS 90
 Db 73 LSISL--DDAFLRLRARKFDYDRAOLQLYNNHGCRRSWPEVSNLRSALKDVLSNG 129

Query 91 SKQDQLRTKMRCEELL-----LQECAHQTTKLGKRVET---ITIYD 129
 Db 130 FLTVLPHTDPRGCCHVLCTRDRWIPSNVPITENRAIVTLEKIQSEETQVNGVILAD 189

Query 130 CEGIGLKLHWKPAVEAYGEFLC---MFEENYPETLKRLFVVKAPKLFVPAVNLKPKFL 184
 Db 190 YKGYSLS----KASHFCBFIARKVIGLQDGPIRKAVHIVNEPRFKGIPAIKPKFL 244

Query 185 SEDTRKTMVGLANYKEVLKHLISPDQ--VPVEYGGMTDPD 224
 Db 245 KEKTAANRFFLHGSDLSSL--HTSLPRNLPKLKEYGGTAGELD 283

RESULT 13

US-09-270-767-32985

Sequence 32985, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQUENCE: PatentIn Ver. 2.0

SEQ ID NO: 32985

LENGTH: 136

TYPE: PRT

ORGANISM: *Drosophila melanogaster*

US-09-270-767-32985

Query Match 5.7%; Score 114.5; DB 2; Length 136;

Best Local Similarity 24.6%; Pred. No. 8e-05;

Matches 33; Conservative 35; Mismatches 49; Indels 17; Gaps 6;

Query 240 PRKTYVRDQVKKQQEH---SVQISRGSSHQVEYETI-LFPGCCVLRQFMSDGAIVFGIF- 294
 Db 1 PEELYYI-DQSSQSDRDFVEAQVPGKGDKLKHFKVNEEQKILSWEFRTEDYDKFGIYS 59

Query 295 LTKMGGERORAGEMTEVLPNQRNYSHLVPEPDGTLTCSDPGIYVNRDFNTYSFIBAKRKY 354
 Db 60 VDDKTEGEKRSVPVLTQVSYB----MDIGYISTRPNTTYVFDNSASYLRSKKLRY 113

Query 355 TVEVLLPDKASEEK 368
 Db 114 WVDLI----SEE 122

RESULT 14
 US-09-270-767-48202
 ; Sequence 48202, Application US/09270767
 ; PARENT NUMBER: 670491
 ; GENERAL INFORMATION
 ; APPLICANT: Homburgir et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 48202
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-48202

Query Match 5.7%; Score 114.5; DB 2; Length 136;
 Best Local Similarity 24.6%; Pred. No. 8e-05; Mismatches 49; Indels 17; Gaps 6;
 Matches 33; Conservative 35; Gapopen 49;

Qy 240 PRKYYVRPQVKQQYEH---SVOIQRSGSSHQEYEI-LPGCVLRLQFMMSDGADVGFGIP- 294
 Db 1 PEEDYY-I-QSSQSQRDVEAQVPKGDRKLKLFKVNVBEQKILSWERTFDDIKGIYS 59

Qy 295 LKTKMGERORAGEMTEVLPNQRYNSHLVPEDGTLTCSDPGIVYLRFDNNTYSFIHAKKVN 354
 Db 60 VDDDTGERRSEVPLGTVSNE-----MDEIGYISTRPNTTYVVPENASYLRSCKLRY 113

Qy 355 TVEVLLPKASEEK 368
 Db 114 WVDLI-----SEEFF 122

RESULT 15
 US-09-244-805-62
 ; Sequence 62, Application US/09244805
 ; Patent No. 6699660
 ; GENERAL INFORMATION:
 ; APPLICANT: Worley, Paul F.
 ; APPLICANT: Lanahan, Anthony
 ; APPLICANT: Goatz, Bernard
 ; APPLICANT: Heimisch, Holger
 ; APPLICANT: Kuner, Rohini
 ; APPLICANT: Scheek, Sigrid
 ; APPLICANT: Nikolic, Karoly
 ; APPLICANT: Zhukowski, Eugene
 ; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
 ; FILE REFERENCE: 10496/004001
 ; CURRENT FILING NUMBER: US/09/244,805
 ; CURRENT FILING DATE: 1999-05-05
 ; PRIOR APPLICATION NUMBER: 60/074,518
 ; PRIOR FILING DATE: 1998-02-12
 ; PRIORITY NUMBER: 60/074,135
 ; PRIORITY NUMBER: 60/074,135
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 62
 ; LENGTH: 342
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-244-805-62

Query Match 5.6%; Score 113; DB 2; Length 342;
 Best Local Similarity 22.9%; Pred. No. 0.00056; Mismatches 74; Indels 32; Gaps 5;
 Matches 41; Conservative 32; Gapopen 74;

Qy 72 PWYDIIGPKDAKGLFSASKQDLRKMRECELL-----LQECAHQT 114
 :: : | : | : | : | : | : | : | : | : | : | :

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OM protein - protein search, using bw model

Run on: May 2, 2006, 18:49:42 ; Search time 165 Seconds
 (without alignments)
 957.209 Million cell updates/sec

Title: US-10-696-699A-2

Perfect score: 2018

Sequence: 1 MSGRYGDLSPRQEAKAPF.....LLPDKASEEKKMQLQAGTPK 378

Scoring table: BL03M62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_AA_Main.*

1: /cgcn2_6_ptodata/1/pubpa/us07_pubcomb.pep:*

2: /cgcn2_6_ptodata/1/pubpa/us08_pubcomb.pep:*

3: /cgcn2_6_ptodata/1/pubpa/us09_pubcomb.pep:*

4: /cgcn2_6_ptodata/1/pubpa/us10_pubcomb.pep:*

5: /cgcn2_6_ptodata/1/pubpa/us11_pubcomb.pep:*

6: /cgcn2_6_ptodata/1/pubpa/us11_pubcomb.pep:*

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	378	4 US-10-419-629-2	Sequence 2, Appli
2	2018	100.0	378	4 US-10-696-699A-2	Sequence 2, Appli
3	1827.5	90.6	403	4 US-10-220-75A-4	Sequence 4, Appli
4	1827.5	90.6	403	4 US-10-419-529-4	Sequence 4, Appli
5	1827.5	90.6	403	4 US-10-072-012-448	Sequence 4, Appli
6	1827.5	90.6	403	4 US-10-696-699A-4	Sequence 4, Appli
7	1827.5	90.6	403	5 US-10-723-060-1875	Sequence 1875, Ap
8	1827.5	90.6	403	5 US-10-73-923-2393	Sequence 22953, A
9	1827.5	90.6	403	5 US-10-73-923-2394	Sequence 22954, A
10	1827.5	90.6	403	5 US-10-631-167-841	Sequence 841, App
11	1827.5	90.6	403	5 US-10-74-237-294	Sequence 294, App
12	1724.5	85.5	403	4 US-10-072-012-450	Sequence 450, App
13	1724.5	85.5	403	5 US-10-732-223-2275	Sequence 22775, A
14	1722.5	85.4	403	4 US-10-220-475A-17	Sequence 2, Appli
15	1722.5	85.4	403	4 US-10-072-012-449	Sequence 449, App
16	1722.5	85.4	403	5 US-10-732-223-2278	Sequence 22778, A
17	1685.5	83.5	403	5 US-10-73-923-2398	Sequence 22958, A
18	1616.5	80.1	387	5 US-10-732-923-2397	Sequence 22957, A
19	1548	76.7	293	4 US-10-696-699A-15	Sequence 15, Appli
20	1428	70.8	400	4 US-10-20-475A-17	Sequence 17, Appli
21	1428	70.8	400	5 US-10-73-923-2396	Sequence 22956, A
22	1423.5	70.5	419	5 US-10-450-763-4364	Sequence 43464, A
23	1413	70.0	400	4 US-10-072-012-451	Sequence 451, App
24	1413	70.0	400	5 US-10-732-923-2278	Sequence 22780, A
25	1309.5	64.9	403	5 US-10-732-923-2277	Sequence 22774, A
26	1304.5	64.6	406	4 US-10-220-475A-18	Sequence 18, Appli
27	1304.5	64.6	406	4 US-10-072-012-447	Sequence 447, App

ALIGNMENTS

RESULT 1
 US-10-419-629-2
 ; Sequence 2, Application US/10419629
 ; Publication No. US2004003915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sanders, Bob G.
 ; APPLICANT: Kline, Kimberly
 ; APPLICANT: Yu, Weiping
 ; APPLICANT: Liu, Hui
 ; APPLICANT: Hartash, Feras
 ; TITLE OF INVENTION: Tocopherol Associated Protein and Uses Thereof
 ; FILE REFERENCE: D6453
 ; CURRENT APPLICATION NUMBER: US/10/419,629
 ; CURRENT FILING DATE: 2003-04-21
 ; PRIORITY NUMBER: US 60/373,870
 ; PRIORITY FILING DATE: 2002-04-19
 ; NUMBER OF SEQ ID NOS: 7
 ; SEQ ID NO: 2
 ; LENGTH: 378
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; OTHER INFORMATION: P2P polypeptide
 US-10-419-629-2

Query Match 100.0%; Score 2018; DB 4; Length 378;
 Best Local Similarity 100.0%; Pred. No. 8-8e-194;
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRVGDLSPRKALAKEASTCRSPRGMSWSSSERLTTSLAWQPPEVQQYL 60
 Db 1 MSGRVGDLSPRKALAKEASTCRSPRGMSWSSSERLTTSLAWQPPEVQQYL 60

QY 1 VETTLYDEBGLGLGHLNKPAAVAYGEFLCMPEENYPETLKRLTVKAKLPVAYNL 180
 Db 1 GGMGYDLDGCPVWYDIIGPKDAAKLLFASQDILTRKRECEILLQEAHQTKLGRK 120
 QY 1 VETTLYDEBGLGLGHLNKPAAVAYGEFLCMFEENYPETLKRLTVKAKLPVAYNL 180
 Db 1 GGMGYDLDGCPVWYDIIGPKDAAKLLFASQDILTRKRECEILLQEAHQTKLGRK 120

QY 1 KPFLESDTRKIMVIGANTYKEVLKLKHISPDQPVPEYGTMTDPDGNPCKCSKINNGDIP 240
 Db 1 KPFLESDTRKIMVIGANTYKEVLKLKHISPDQPVPEYGTMTDPDGNPCKCSKINNGDIP 240

QY 1 VETTLYDEBGLGLGHLNKPAAVAYGEFLCMFEENYPETLKRLTVKAKLPVAYNL 180
 Db 1 VETTLYDEBGLGLGHLNKPAAVAYGEFLCMFEENYPETLKRLTVKAKLPVAYNL 180

RESULT 2
 US-10-696-699A-2
 ; Sequence 2, Application US/10696699A
 ; Publication No. US20040152883A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sanders, Bob G.
 ; APPLICANT: Kline, Kimberly
 ; APPLICANT: Yu, Weiping
 ; APPLICANT: Liu, Hui
 ; APPLICANT: Hantash, Feras
 ; TITLE OF INVENTION: Tocopherol Associated Protein and Uses Thereof
 ; FILE REFERENCE: D6153CIP
 ; CURRENT APPLICATION NUMBER: US/10/696,699A
 ; CURRENT FILING DATE: 2003-10-29
 ; PRIOR APPLICATION NUMBER: US 10/419,629
 ; PRIOR FILING DATE: 2003-04-21
 ; NUMBER OF SEQ ID NOS: 19
 ; SEQ ID NO 2
 ; LENGTH: 378
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; OTHER INFORMATION: TAP-38 polypeptide
 ; US-10-696-699A-2

Query Match 100.0%; Score 2018; DB 4; Length 378;
 Best Local Similarity 100.0%; Pred. No. 8.8e-194;
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGRVDLSPROKEALAKEASTCRSPCSCGMWSSSKRSKTLTSLAWQPPEVIOYLS 60
 Db 1 MSGRVDLSPROKEALAKEASTCRSPCSCGMWSSSKRSKTLTSLAWQPPEVIOYLS 60

Qy 61 GGNCGYDLDGCPWYDIIGPKDAKGILFASAKDQLLPTKMRCECELLQECAHOTTKLGRK 120
 Db 61 GGNCGYDLDGCPWYDIIGPKDAKGILFASAKDQLLPTKMRCECELLQECAHOTTKLGRK 120

Qy 121 VETITIIDCCEGLKLHMKPAVEAYGFGLCNFEENYETKLRLFVVKAPKLFPVAYNL 180
 Db 121 VETITIIDCCEGLKLHMKPAVEAYGFGLCNFEENYETKLRLFVVKAPKLFPVAYNL 180

Qy 181 KPFLESDTRKKINVLGANYKEVLLKHTSPDQVPEVYGGTTMDDGPKCKSKINYGGDIP 240
 Db 181 KPFLESDTRKKINVLGANYKEVLLKHTSPDQVPEVYGGTTMDDGPKCKSKINYGGDIP 240

Qy 241 RKYYVRDQKQOYEHSVQISRGSSHOVYEILFPGCVLRWQFMSDGAQVGFJFLKTNGM 300
 Db 241 RKYYVRDQKQOYEHSVQISRGSSHOVYEILFPGCVLRWQFMSDGAQVGFJFLKTNGM 300

Qy 301 ERORAGENTEVLPNQRYNSHLVPEDGTITCSDPGIVYLRFDNTYSFTHAKKNFTVEVLL 360
 Db 301 ERORAGENTEVLPNQRYNSHLVPEDGTITCSDPGIVYLRFDNTYSFTHAKKNFTVEVLL 360

Qy 361 PDKAEEBMKQLGAGTPK 378
 Db 361 PDKAEEBMKQLGAGTPK 378

RESULT 3
 US-10-220-475A-4
 ; Sequence 4, Application US/10220475A
 ; Publication No. US20040023227A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INOUE, KEIZO
 ; APPLICANT: ARAI, HIROYUKI
 ; TITLE OF INVENTION: DNA ENCODING SQUALENE EPOXIDASE-PROMOTING FACTOR
 ; FILE REFERENCE: 04853_0096-00000
 ; CURRENT APPLICATION NUMBER: US/10/220,475A
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: PCT/JP01/01592
 ; PRIOR FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: JP 2000-57743
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-220-475A-4

Query Match 90.6%; Score 1827.5; DB 4; Length 403;
 Best Local Similarity 87.1%; Pred. No. 1.4e-174;
 Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;

Qy 1 MSGRVDLSPROKEALAKFRENVOQVLPALPNPDYFLRLMLRARSFDLQSEALRKHV 95
 Db 1 MSGRVDLSPROKEALAKFRENVOQVLPALPNPDYFLRLMLRARSFDLQSEALRKHV 96
 Qy 40 ||| KPLTTSAAQWQPPEVIOYLSGCGMCYDLDGCPWYD1GPKDAKGILFASAKDQ 100
 Db 61 EPRKQKPIDNTISWPPEVIOYLSGCGMCYDLDGCPWYD1GPKDAKGILFASAKDQ 120
 Qy 96 LRTKMECECELLQECAHOTTKLGRKVETITIYDCERGLGIKHLWKPDAVEAYGFCLCMFEE 155
 Db 121 LRTKMECECELLQECAHOTTKLGRKVETITIYDCERGLGIKHLWKPDAVEAYGFCLCMFEE 180

Qy 156 NYPETKLRLFVVKAPKLFPVAYNLKPFLESDTRKKINVLGANYKEVLLKHTSPDQVPE 215
 Db 181 NYPETKLRLFVVKAPKLFPVAYNLKPFLESDTRKKINVLGANYKEVLLKHTSPDQVPE 240

Qy 216 YGGTMDDPGNPCKSKINYGGDIPKXXYYDQVHQEYHSVQISRGSSHOVYEILFPG 275
 Db 241 YGGTMDDPGNPCKSKINYGGDIPKXXYYDQVHQEYHSVQISRGSSHOVYEILFPG 300

Qy 276 CVLRWQFMSDGAQVGFJFLKTNGMGERQRAGEMTEVLPNQRYNSHLVPEDGTITCSDPG 335
 Db 301 CVLRWQFMSDGAQVGFJFLKTNGMGERQRAGEMTEVLPNQRYNSHLVPEDGTITCSDPG 360

Qy 336 YVLRFDNTYSFTHAKKNFTVEVLLPDKASEEKMKGQRAQEMTEVLPNQRYNSHLVPEDGTITCSDPG 378
 Db 361 YVLRFDNTYSFTHAKKNFTVEVLLPDKASEEKMKGQRAQEMTEVLPNQRYNSHLVPEDGTITCSDPG 403

RESULT 4
 US-10-419-629-4
 ; Sequence 4, Application US/10419629
 ; Publication No. US20040023915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sanders, Bob G.
 ; APPLICANT: Kline, Kimberly
 ; APPLICANT: Yu, Weiping
 ; APPLICANT: Liu, Hui
 ; APPLICANT: Hantash, Feras
 ; TITLE OF INVENTION: Tocopherol Associated Protein and uses thereof
 ; FILE REFERENCE: D6453
 ; CURRENT APPLICATION NUMBER: US/10/419,629
 ; CURRENT FILING DATE: 2003-04-21
 ; PRIOR APPLICATION NUMBER: US 60/373,870
 ; PRIOR FILING DATE: 2002-04-19
 ; NUMBER OF SEQ ID NOS: 7
 ; SEQ ID NO 4
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

FEATURE: NAME/KEY: PEPTIDE
 OTHER INFORMATION: TAP-46 polypeptide
 US-10-419-699-4

Query Match 90.6%; Score 1827.5; DB 4; Length 403;
 Best Local Similarity 87.1%; Pred. No. 1..e-174;
 Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;

Qy 1 MSGRVGDSLSPROKEALAK<----->PEASTCRSRPCSGSMWSSS----- 39
 Db 1 MSGRVGDSLSPROKEALAKPREFNTQDVLPA LPNDDFYTLRWRARSFLQKSEAMLRKRVH 60

Qy 40 ----KRTLTTSLAWQPPEVIIQQLTGCGYDLDGCPWYD1GPKDKAGLFLSASKD L 95
 Db 61 EFRKQKDIDN1ISQQPPEVIIQQLTGCGYDLDGCPWYD1GPKDKGLLPSASKD L 120

Qy 96 LRTKRECELLQECAHQTTLGRKVETITIYDCBGLGLKHLWKPAVEAYGEFLCMFEE 155
 Db 121 LRTKRECELLQECAHQTTLGRKVETITIYDCBGLGLKHLWKPAVEAYGEFLCMFEE 180

Qy 156 NYPETKLRLFPVKAPKLFPVAYNLKPFUSEDTRKKMVLYKANKEVTLKHLGK 215
 Db 181 NYPETKLRLFPVKAPKLFPVAYNLKPFUSEDTRKKMVLYKANKEVTLKHLGK 240

Qy 216 YGGTMTDPGNPKCKSKINYGGDLPRKYYDRDQVKQOYERSVOTRGSSHHQVEYEILFG 275
 Db 241 YGGTMTDPGNPKCKSKINYGGDLPRKYYDRDQVKQOYERSVOTRGSSHHQVEYEILFG 300

Qy 276 CVERWQMSDGA DVGFGIPLKTKRNGERQRAGEMTEVLPNQRYNSHLVPEDGTLLTCSDPGI 335
 Db 301 CVERWQMSDGA DVGFGIPLKTKRNGERQRAGEMTEVLPNQRYNSHLVPEDGTLLTCSDPGI 360

Qy 336 YVLRFDTNTYSFIHAKKVNFTVEVLLPDKA SEEKMQLGAGTPK 378
 Db 361 YVLRFDTNTYSFIHAKKVNFTVEVLLPDKA SEEKMQLGAGTPK 403

RESULT 5
 US-10-072-012-448
 ; Sequence 448, Application US/10072012
 ; Publication No. US/00-003393A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tchertnev, Velizar
 ; APPLICANT: Spycek, Kimberly
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shimek, Richard
 ; APPLICANT: Li, Li
 ; APPLICANT: Gangolli, Esha
 ; APPLICANT: Padgett, Muralidhara
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Taupier Jr., Raymond J.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Colman, Steven D.
 ; APPLICANT: Wolenc, Adam R.
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Furtak, Katarzyna
 ; APPLICANT: Grosser, William M.
 ; APPLICANT: Alsobrook II, John P.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Burgess, Catherine B.
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-258
 ; CURRENT APPLICATION NUMBER: US/10/072,012
 ; CURRENT FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,102
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,517
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,412
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,395
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/266,406
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 60/266,767
 ; PRIOR FILING DATE: 2001-02-05
 ; PRIOR APPLICATION NUMBER: 60/267,057
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: 60/266,975
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: 60/267,459
 ; PRIOR FILING DATE: 2001-02-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1391
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 448
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-072-012-448

Query Match 90.6%; Score 1827.5; DB 4; Length 403;
 Best Local Similarity 87.1%; Pred. No. 1..e-174;
 Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;

Qy 1 MSGRVGDSLSPROKEALAK<----->PEASTCRSRPCSGSMWSSS----- 39
 Db 1 MSGRVGDSLSPROKEALAKPREFNTQDVLPA LPNDDFYTLRWRARSFLQKSEAMLRKRVH 60

Qy 40 ----KRTLTTSLAWQPPEVIIQQLTGCGYDLDGCPWYD1GPKDKAGLFLSASKD L 95
 Db 61 EFRKQKDIDN1ISQQPPEVIIQQLTGCGYDLDGCPWYD1GPKDKGLLPSASKD L 120

Qy 96 LRTKRECELLQECAHQTTLGRKVETITIYDCBGLGLKHLWKPAVEAYGEFLCMFEE 155
 Db 121 LRTKRECELLQECAHQTTLGRKVETITIYDCBGLGLKHLWKPAVEAYGEFLCMFEE 180

Qy 156 NYPETKLRLFPVKAPKLFPVAYNLKPFUSEDTRKKMVLYKANKEVTLKHLGK 215
 Db 181 NYPETKLRLFPVKAPKLFPVAYNLKPFUSEDTRKKMVLYKANKEVTLKHLGK 240

Qy 216 YGGTMTDPGNPKCKSKINYGGDLPRKYYDRDQVKQOYERSVOTRGSSHHQVEYEILFG 275
 Db 241 YGGTMTDPGNPKCKSKINYGGDLPRKYYDRDQVKQOYERSVOTRGSSHHQVEYEILFG 300

Qy 276 CVERWQMSDGA DVGFGIPLKTKRNGERQRAGEMTEVLPNQRYNSHLVPEDGTLLTCSDPGI 335
 Db 301 CVERWQMSDGA DVGFGIPLKTKRNGERQRAGEMTEVLPNQRYNSHLVPEDGTLLTCSDPGI 360

Qy 336 YVLRFDTNTYSFIHAKKVNFTVEVLLPDKA SEEKMQLGAGTPK 378
 Db 361 YVLRFDTNTYSFIHAKKVNFTVEVLLPDKA SEEKMQLGAGTPK 403

RESULT 6
 US-10-696-699A-4
 ; Sequence 4, Application US/10696699A
 ; Publication No. US/2004015883A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sanders, Bob G.
 ; APPLICANT: Kline, Kimberly
 ; APPLICANT: Yu, Weiping
 ; APPLICANT: Liu, Hui
 ; APPLICANT: Hanash, Feras
 ; TITLE OF INVENTION: Tocopherol Associated Protein and Uses Thereof
 ; FILE REFERENCE: D645AC1
 ; CURRENT APPLICATION NUMBER: US/10/696,699A
 ; CURRENT FILING DATE: 2003-10-29

PRIOR APPLICATION NUMBER: US 10/419,629
 PRIORITY FILING DATE: 2003-04-21
 NUMBER OF SEQ ID NOS: 19
 SEQ ID NO 4
 LENGTH: 403
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: PEPTIDE TAP-46 polypeptide
 OTHER INFORMATION: TAP-46 polypeptide
 US-10-696-699a-4

Query Match 90.6%; Score 1827.5; DB 5; Length 403;
 Best Local Similarity 87.1%; Pred. No. 1.4e-174;
 Indels 25; Gaps 2;

Db 1 MSGRVGDLSPROKEALAKFRENVQDVLPALPNPDDYFLRLRARRSFQKSEMLRKHV 60
 Qy 40 ---KRTLTLTSLAWQPPEVIOYLQSGMCGYDLDGCPWVYD1GPKDAGKGLFSASKDL 95
 Db 61 EFRKQDIDNTISWPPEVIOYLQSGMCGYDLDGCPWVYD1GPKDAGKGLFSASKDL 120
 Qy 96 LRTKMRCECELLQECAHOTTKLGRKVETITIYDCEGLGLKHLWKPAVEAYGEFLCMFEE 155
 Db 121 LRTKMRCECELLQECAHOTTKLGRKVETITIYDCEGLGLKHLWKPAVEAYGEFLCMFEE 180
 Qy 156 NYPETLKRFLVVKAPKLFPVAYNLKPFLSEDTRKKIMVLGANYKEVLLKHSIPDQVPE 215
 Db 181 NYPETLKRFLVVKAPKLFPVAYNLKPFLSEDTRKKIMVLGANWKEVLLKHSIPDQVPE 240
 Qy 216 YGGTMTDPDGNPKCKSKINYGGDIPKRYYYDQVHQOYEHSVQISRGSSHOVEYEILFPG 275
 Db 241 YGGTMTDPDGNPKCKSKINYGGDIPKRYYYDQVHQOYEHSVQISRGSSHOVEYEILFPG 300
 Qy 276 CYLRWFQMSDGADEVGFGLYFKTKMGERQRAGEMTEYLPNQRYNSHLYPEDGTLTCSDPGI 335
 Db 301 CYLRWFQMSDGADEVGFGLYFKTKMGERQRAGEMTEYLPNQRYNSHLYPEDGTLTCSDPGI 360
 Qy 336 YVLRFDTNTYSPTHAKCUNFTVVELLPDKASEEKMQLGAGTPK 378
 Db 361 YVLRFDTNTYSPTHAKCUNFTVVELLPDKASEEKMQLGAGTPK 403

RESULT 8
 US-10-732-923-22953
 Sequence 22953, Application US/10732923
 Publication No. US20050108791A1
 GENERAL INFORMATION:
 APPLICANT: Edgerton, Michael D
 TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 FILE REFERENCE: 38-15 (52796)
 CURRENT APPLICATION NUMBER: US/10/732,923
 CURRENT FILING DATE: 2003-12-10
 PRIOR APPLICATION NUMBER: US/10/732,923
 PRIOR FILING DATE: 2002-12-04
 NUMBER OF SEQ ID NOS: 24149
 SEQ ID NO 22953
 LENGTH: 403
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-732-923-22953

Query Match 90.6%; Score 1827.5; DB 5; Length 403;
 Best Local Similarity 87.1%; Pred. No. 1.4e-174;
 Indels 25; Gaps 2;

Db 1 MSGRVGDLSPROKEALAKFRENVQDVLPALPNPDDYFLRLRARRSFQKSEMLRKHV 60
 Qy 40 ---KRTLTLTSLAWQPPEVIOYLQSGMCGYDLDGCPWVYD1GPKDAGKGLFSASKDL 95
 Db 61 EFRKQDIDNTISWPPEVIOYLQSGMCGYDLDGCPWVYD1GPKDAGKGLFSASKDL 120
 Qy 96 LRTKMRCECELLQECAHOTTKLGRKVETITIYDCEGLGLKHLWKPAVEAYGEFLCMFEE 155
 Db 121 LRTKMRCECELLQECAHOTTKLGRKVETITIYDCEGLGLKHLWKPAVEAYGEFLCMFEE 180
 Qy 156 NYPETLKRFLVVKAPKLFPVAYNLKPFLSEDTRKKIMVLGANYKEVLLKHSIPDQVPE 215
 Db 181 NYPETLKRFLVVKAPKLFPVAYNLKPFLSEDTRKKIMVLGANWKEVLLKHSIPDQVPE 240
 Qy 216 YGGTMTDPDGNPKCKSKINYGGDIPKRYYYDQVHQOYEHSVQISRGSSHOVEYEILFPG 275
 Db 241 YGGTMTDPDGNPKCKSKINYGGDIPKRYYYDQVHQOYEHSVQISRGSSHOVEYEILFPG 300
 Qy 276 CYLRWFQMSDGADEVGFGLYFKTKMGERQRAGEMTEYLPNQRYNSHLYPEDGTLTCSDPGI 335

Db	301	CYLRWQFMSGADVGRIFLKTKMGERQRAGEMTEVLPNQRYNSHIVPEDGTLTCSDPGI	366
Qy	336	YVLRFDNTYSFHAKKVNFTVEVLPLDKASEEKMVKOLGAGTPK	378
Db	361	YVLRFDNTYSFHAKKVNFTVEVLPLDKASEEKMVKOLGAGTPK	403
RESULT 9			
US-10-732-923-22954	Sequence 22954	Application US/10732923	
;	Publication No.	US20050108791A1	
;	GENERAL INFORMATION:		
;	APPLICANT:	Egerton, Michael D	
;	TITLE OF INVENTION:	TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES	
;	FILE REFERENCE:	38-15(52796)C	
;	CURRENT APPLICATION NUMBER:	US/10/732, 923	
;	CURRENT FILING DATE:	2003-12-10	
;	PRIOR APPLICATION NUMBER:	10/310, 154	
;	PRIOR FILING DATE:	2003-12-04	
;	NUMBER OF SEQ ID NOS:	24149	
;	SEQ ID NO:	2954	
;	LENGTH:	403	
;	TYPE:	PRT	
;	ORGANISM:	Homo sapiens	
US-10-732-923-22954			
Query	Match	90.6%	Score 1827.5; DB 5; Length 403;
Best	Local Similarity	87.1%	Pred. No. 1.4e-174;
Matches	351; Conservative	9; Mismatches 18; Indels 25; Gaps 2;	
;	MSGRVGDLSPRQEALAK-	-----PEASTCRSRPSCGSMWSES-----	39
Qy	1	MSGRVGDLSPRQEALAK-	-----PEASTCRSRPSCGSMWSES-----
Db	1	MSGRVGDLSPRQEALAKFRENTQDVLPALPNPDYFLLRWLRAESFDLQSEAMLRKHV	60
Qy	40	-----KRTLTTSLAWQPPEVIOYLSSGMCGYLDGCPWYD1IGPKDAKGLLFSASKQDL	95
Db	61	EPRKQKDIDNITISWPQPEVIOYLSSGMCGYD1DGCWPWYD1GPKDAKGLLFSASKQDL	120
Qy	96	LRTKMPRECCELLQCAHOTTKLGRKVETIITYDCEGIGLKLHWKDAVEAGEFLCMFEE	155
Db	121	LRTKMPRECCELLQCAHOTTKLGRKVETIITYDCEGIGLKLHWKDAVEAGEFLCMFEE	180
Qy	156	NYPETLKRFLFVVKAPKLFPPVATNLIKPFLSEDTRKTMVGLANYKEVTLRKHISPDQPVVE	215
Db	181	NYPETLKRFLFVVKAPKLFPPVATNLIKPFLSEDTRKTMVGLANWKEVTLRKHISPDQPVVE	240
Qy	216	YGGTMTDDGNPKCSKLNNGGDI PRKCYVRDQVKQOYEHSHVQI SRGSSHQVEYEILFPG	275
Db	241	YGGTMTDDGNPKCSKLNNGGDI PRKCYVRDQVKQOYEHSHVQI SRGSSHQVEYEILFPG	300
Qy	276	CYLRWQFMSGADVGFGFLKTKMGERQRAGEMTEVLPNQRYNSHIVPEDGTLTCSDPGI	335
Db	301	CYLRWQFMSGADVGFGFLKTKMGERQRAGEMTEVLPNQRYNSHIVPEDGTLTCSDPGI	360
Qy	336	YVLRFDNTYSFHAKKVNFTVEVLPLDKASEEKMVKOLGAGTPK	378
Db	361	YVLRFDNTYSFHAKKVNFTVEVLPLDKASEEKMVKOLGAGTPK	403
RESULT 10			
US-10-631-467-841	Sequence 841	Application US/10631467	
;	Publication No.	US2005020496A1	
;	GENERAL INFORMATION:		
;	APPLICANT:	Genox Research Inc.	
;	TITLE OF INVENTION:	disease	
;	FILE REFERENCE:	3462-1005-000	
;	CURRENT APPLICATION NUMBER:	US/10/631,467	
;	CURRENT FILING DATE:	2003-07-31	
;	PRIOR APPLICATION NUMBER:	JP 2003-077212	
;	PRIOR FILING DATE:	2003-03-20	
;	DRUG DEPARTMENT:	NTMNP	
;	DRUG DEPARTMENT NUMBER:	JP 2002-2293112	

Qy 1 MSGRVGDLSPROKEALAK-----PEASTCRSRPCSGSMWSSSES----- 39
 Db 1 MSGRVGDLSPROKEALAKFRENQDVPLTLPLPNDDYFLRLWRARSPLQLKSBEAMLRKHV 60

Qy 40 ---- KRTLTTSLAWQPEVIOQYLGGCNGCYDLDGCPTWYDINGPKDAKGLLFSASKQDL 95
 Db 61 EFRKQDKIDKISWQPEVIOQYLGGCGYDLDGCPTWYDINGPKDAKGLLFSASKQDL 120

Qy 96 LRTKMRCELLQCAHQTTLGRKVTTIYDCEGLKLKHWKPAVAYGEFLCMFEE 155
 Db 121 LRTKMRCELLQCAHQTTLGRKVTTIYDCEGLKLKHWKPAVAYGEFLCMFEE 180

Qy 156 NYPETLKLRFVVKAPKLFPVAYNLKPFLSEDTRKVNVLGANYKEVLLKHISPDQVPE 215
 Db 181 NYPETLKLRFVVKAPKLFPVAYNLKPFLSEDTRKVNVLGAWKVEVLLKHISPDQLVK 240

Qy 216 YGGTMTDPGNPCKSKINCKGDIPIKTYVRDQVKQOEHSYQISRGSSSHQVEYEILFPG 275
 Db 241 YGGTMTDPGNPCKSKINCKGDIPIKTYVRDQVKQOEHSYQISRGSSSHQVEYEILFPG 300

Qy 276 CVLRWFMSDGAQDVGFGIFLKTKMGERQRAGEMTEVLPNQRYNSHLVPEDGTLTCSDPGI 335
 Db 301 CVLRWFMSDGAQDVGFGIFLKTKMGERQRAGEMTEVLPNQRYNSHMVPEDGTLTCSEGI 360

Qy 336 YVLFEDNTYSFTHAKVNFNTYEVLPLPKASEEKMKGAGTPK 378
 Db 361 YVLFEDNTYSFTHAKVSFTEVLPLPKAAEKLNOQGAVTPK 403

RESULT 15
 US-10-072-012-449
 Sequence 449, Application US/10072012
 Publication No. US20040033493A1
 GENERAL INFORMATION:
 / APPLICANT: tchernev, Velizar
 / SPYTEK, Kimberly
 / APPLICANT: Zerhusen, Bryan
 / APPLICANT: Paturajan, Meera
 / APPLICANT: Shirkers, Richard
 / APPLICANT: Li, Li
 / APPLICANT: Gangolli, Esha
 / APPLICANT: Padigaru, Muralidhara
 / APPLICANT: Anderson, David W.
 / APPLICANT: Rastelli, Luca
 / APPLICANT: Miller, Charles E.
 / APPLICANT: Gerlach, Valerie
 / APPLICANT: Traupier Jr, Raymond J.
 / APPLICANT: Gushev, Vladimir Y.
 / APPLICANT: Colman, Steven D.
 / APPLICANT: Wolenc, Adam R.
 / APPLICANT: Pena, Carol E. A.
 / APPLICANT: Furtak, Katarzyna
 / APPLICANT: Grossbe, William M.
 / APPLICANT: Alsobrook II, John P.
 / APPLICANT: Lesley, Denise M.
 / APPLICANT: Rieger, Daniel K.
 / APPLICANT: Burgess, Catherine E.
 / TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 / FILE REFERENCE: 21402-258
 / CURRENT APPLICATION NUMBER: US/10/072,012
 / PRIORITY FILING DATE: 2002-01-31
 / PRIOR APPLICATION NUMBER: 60/265,102
 / PRIORITY FILING DATE: 2001-01-30
 / PRIOR APPLICATION NUMBER: 60/265,514
 / PRIORITY FILING DATE: 2001-01-31
 / PRIOR APPLICATION NUMBER: 60/265,517
 / PRIORITY FILING DATE: 2001-01-31
 / PRIOR APPLICATION NUMBER: 60/265,412
 / PRIORITY FILING DATE: 2001-01-31
 / PRIOR APPLICATION NUMBER: 60/265,395
 / PRIORITY FILING DATE: 2001-02-02
 / PRIOR FILING DATE: 2001-02-05
 / PRIOR APPLICATION NUMBER: 60/267,057
 / PRIORITY FILING DATE: 2001-02-07
 / PRIOR FILING DATE: 2001-02-07
 / PRIOR APPLICATION NUMBER: 60/266,975
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 1391
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 449
 / LENGTH: 403
 / TYPE: PRT
 / ORGANISM: Rattus norvegicus

Query Match 85.4%; Score 1722.5; DB 4; Length 403;
 Best Local Similarity 81.1%; Pred. No. 5.2e-164;
 Matches 327; Conservative 25; Mismatches 26; Indels 25; Gaps 2;

Qy 1 MSGRVGDLSPROKEALAK-----PEASTCRSRPCSGSMWSSSES----- 39
 Db 1 MSGRVGDLSPROKEALAKFRENQDVPLALPNDDYFLRLWRARSFLOKSEAMLRKHV 60

Qy 40 ---- KRTLTTSLAWQPEVIOQYLGGCNGCYDLDGCPTWYDINGPKDAKGLLFSASKQDL 95
 Db 61 EFRKQDKIDKISWQPEVIOQYLGGCGYDLDGCPTWYDINGPKDAKGLLFSASKQDL 120

Qy 96 LRTKMRCELLQCAHQTTLGRKVTTIYDCEGLKLKHWKPAVAYGEFLCMFEE 155
 Db 121 LRTKMRCELLQCAHQTTLGRKVTTIYDCEGLKLKHWKPAVAYGEFLCMFEE 180

Qy 156 NYPETLKLRFVVKAPKLFPVAYNLKPFELSEDTRKVNVLGANYKEVLLKHISPDQVPE 215
 Db 181 NYPETLKLRFVVKAPKLFPVAYNLKPFELSEDTRKVNVLGANYKEVLLKHISPDQVPE 240

US-10-072-012-449

Query Match 85.4%; Score 1722.5; DB 4; Length 403;
 Best Local Similarity 81.1%; Pred. No. 5.2e-164;
 Matches 327; Conservative 25; Mismatches 26; Indels 25; GapB 2;

Qy 1 MSGRVGDSLSPROKELAK-----PEASTCRSRRPCSGSMWSSES---- 39
 Db 1 MSGRVGDSLSPKQEALAKFRENQDVLAALPNPDDYFLRWRARSPLQKSEAMIRKRV 60

Qy 40 ---KRITLTSLAWQPPEVIOQYLGGMCCYDLDGCPWYD1GPKDAKGILFSASKDL 95
 :: :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 61 EPRKQDKDIDK1TSWQPPEVIOQYLGGRCGYDLDGCPWYD1GPKDAKGILFSASKDL 120

Qy 96 LRTKMRDRCELLQOCCTQATAKGKKIETITMYDCGGILRHLWKPAVEAGEFLTMPE 155
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 121 LRTKMRDRCELLQOCCTQATAKGKKIETITMYDCGGILRHLWKPAVEAGEFLTMPE 180

Qy 156 NYPTLKRLFKVVKAPKLFPVAYNLKPFLSEDTRKK1MVLGANKEYLVHISPDQYVE 215
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 181 NYPTLKRLFVVKAPKLFPVANLIKPLSEDTRKK1MVLGANKEYLVHISPDQYVE 240

Qy 216 YGGTMTDDGNDGPKCKSKINYGGDIPRKYVVDQVKQOQYEHSTQISRGSSHQVEYEILFPG 275
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 241 YGGTMTDDGNDGPKCKSKINYGGDIPKQYVVDQVKQOQYEHSTQISRGSSHQVEYEILFPG 300

Qy 276 CVLRQFNSDGAUFGFLKTKMGERORAGENTEVELNQRNINSHLYPEDGLTCSDPGI 335
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 301 CVLRQFNSEGSDVFGFLKTKMGERORAGENTEVELNQRNINSHYPEDGLTCSDPGI 360

Qy 336 YVLRFDNTYSFIHAKVNTFTVEYLDPDIAKSEENKMKOLGAGTPK 378
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 361 YVLRFDNTYSFIHAKVSEFTVEVLLPDRAAEERLNQQAVTPK 403

Search completed: May 2, 2006, 18:53:26
 Job time : 166 secs

GenCore version 5.1.7
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Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.7	US-10-696-699A-2	Sequence 32081, A
run on:	May 2, 2006, 18:50:52 ; Search time 27 Seconds (without alignments) 636,690 Million cell updates/sec	Sequence 27860, A	Sequence 27859, A
title:	US-10-696-699A-2	Sequence 27858, A	Sequence 27858, A
perfect score:	2018	Sequence 7476, A	Sequence 7476, A
sequence:	1 MSGRVRGDLSPROKBEALAKEP.....LLPDKASEERKMKQLGAGTPK 378	Sequence 16949, A	Sequence 16949, A
scoring table:	BLOSUM62	Sequence 16948, A	Sequence 16948, A
	Gapext 0.5	Sequence 6162, A	Sequence 6162, A
searched:	232119 seqs, 4547862 residues	Sequence 5884, A	Sequence 5884, A
total number of hits satisfying chosen parameters:	232119	Sequence 26460, A	Sequence 26460, A
minimum DB seq length:	0	Sequence 26459, A	Sequence 26459, A
maximum DB seq length:	200000000	Sequence 18644, A	Sequence 18644, A
minimum DB seq length:	0	Sequence 18887, A	Sequence 18887, A
maximum DB seq length:	200000000	Sequence 18886, A	Sequence 18886, A
minimum DB seq length:	0	Sequence 13413, A	Sequence 13413, A
maximum DB seq length:	200000000	Sequence 13411, A	Sequence 13411, A
minimum DB seq length:	0	Sequence 1922, A	Sequence 1922, A
maximum DB seq length:	200000000	Sequence 10781, A	Sequence 10781, A
minimum DB seq length:	0	Sequence 1647, A	Sequence 1647, A
maximum DB seq length:	200000000	Sequence 308, A	Sequence 308, A
minimum DB seq length:	0	Sequence 3617, A	Sequence 3617, A
maximum DB seq length:	200000000	Sequence 10493, A	Sequence 10493, A

post-processing: Minimum Match 0% Maximum Match 100%

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IMMAPTES

result	No.	Query			DB	ID	Description
		Score	Match	Length			
1	1822.5	90.6	403	9	US-10-528-031-7		Sequence 7, App Sequence 2798,
2	1272	63.0	391	11	US-11-072-512-2798		Sequence 3609,
3	1118	55.4	360	11	US-11-072-512-3609		Sequence 7798,
4	233	11.5	463	11	US-11-096-568A-7798		Sequence 7797,
5	233	11.5	479	11	US-11-096-568A-7797		Sequence 7796,
6	233	11.5	483	11	US-11-096-568A-7796		Sequence 28170,
7	222.5	11.0	478	11	US-11-096-568A-28170		Sequence 28169,
8	221.5	11.0	517	11	US-11-096-568A-28168		Sequence 28168,
9	221.5	11.0	558	11	US-11-096-568A-28168		Sequence 32080,
10	216	10.7	409	11	US-11-096-568A-32080		Sequence 32079,
11	216	10.7	433	11	US-11-096-568A-32079		Sequence 27441,
12	214	10.6	511	11	US-11-096-568A-27441		Sequence 27440,
13	214	10.6	551	11	US-11-096-568A-27440		Sequence 27439,
14	214	10.6	560	11	US-11-096-568A-27439		Sequence 9415,
15	213	10.6	394	11	US-11-096-568A-9415		Sequence 9414,
16	213	10.6	423	11	US-11-096-568A-9414		Sequence 9413,
17	206	10.6	449	11	US-11-096-568A-26554		Sequence 26553,
18	206	10.2	443	11	US-11-096-568A-26553		Sequence 18642,
19	206	10.2	463	11	US-11-096-568A-18643		Sequence 26552,
20	206	10.2	485	11	US-11-096-568A-26552		Sequence 26551,

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RESULT 1          Query M...
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; Sequence       Matches
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; GENERAL        Db
; APPLIC        Qy
; APPLIC        Db
; APPLIC        Qy
; APPLIC        Db
; TITLE Q      Qy
; FILE R...      Db
; CURRENT       Qy
; NUMBER        Db
; SOFTWARE      Qy
; SEQ_ID 1      Db
; LENGTH        Qy
; TYPE:         Db
; ORGAN:        Qy
US-10-528        Db

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ALIGNMENTS

22	204	10.1	341	11	US-11-096-568A-#2081	Sequence 32081, A
23	199.5	9.9	546	11	US-11-096-568A-#2860	Sequence 27860, A
24	199.5	9.9	550	11	US-11-096-568A-#2859	Sequence 27859, A
25	199.5	9.9	554	11	US-11-096-568A-#27858	Sequence 27858, A
26	196	9.7	364	11	US-11-087-099-#7476	Sequence 7476, AP
27	193.5	9.6	313	11	US-11-096-568A-#16949	Sequence 16949, AP
28	193.5	9.6	520	11	US-11-096-568A-#16948	Sequence 16948, AP
29	186.5	9.2	302	11	US-11-087-099-#6162	Sequence 6162, AP
30	176.5	8.7	497	11	US-11-087-099-#5884	Sequence 5884, AP
31	176	8.7	137	11	US-11-096-568A-#26460	Sequence 26460, A
32	176	8.7	156	11	US-11-096-568A-#24559	Sequence 26459, A
33	173.5	8.6	430	11	US-11-096-568A-#18644	Sequence 18644, A
34	158	7.8	247	11	US-11-087-099-#5238	Sequence 5238, AP
35	149	7.4	307	11	US-11-096-568A-#18887	Sequence 18887, A
36	149	7.4	309	11	US-11-096-568A-#18886	Sequence 18886, A
37	142.5	7.1	208	11	US-11-096-568A-#13413	Sequence 13413, A
38	142.5	7.1	255	11	US-11-096-568A-#13412	Sequence 13412, A
39	142.5	7.1	289	11	US-11-096-568A-#13411	Sequence 13411, A
40	142	7.0	259	11	US-11-087-099-#1922	Sequence 1922, AP
41	141	7.0	254	11	US-11-087-099-#10781	Sequence 10781, A
42	141	7.0	261	11	US-11-087-099-#1647	Sequence 1647, AP
43	140.5	7.0	255	11	US-11-087-099-#308	Sequence 308, APP
44	140	6.9	256	11	US-11-087-099-#3617	Sequence 3617, APP
45	140	6.9	256	11	US-11-087-099-#10493	Sequence 10493, A

Db 241 YGGTMTDDGPKCKSKINYGGDI PRKXYVRDQVKQQYEHSYQISRGSSHOVEYEILFPG 300
 Qy 276 CVALWQTMPSDGADEVGFIFLKXMGFGEQRAGEMTEVLPNQRNNSHLVPEDTLTCSDPGI 335
 Db 301 CVALWQTMPSDGADEVGFIFLKXMGFGEQRAGEMTEVLPNQRNNSHLVPEDTLTCSDPGI 360
 Qy 336 YVLFDFNTYSFTHAKKVNFTVEVLLPKASEEKMKGQLGAGTP 378
 Db 361 YVLFDFNTYSFTHAKKVNFTVEVLLPKASEEKMKGQLGAGTP 403

RESULT 2

US-11-072-512-2798
 ; Sequence 2798, Application US/11072512
 ; Publication No. US20060029945A1
 GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROTOKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUKIKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOKIKO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOKI
 ; APPLICANT: NAGABARI, KENJI
 ; APPLICANT: MASUBO, YASUHIKO
 ; APPLICANT: MASHO, YASHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: 084335-0191
 CURRENT APPLICATION NUMBER: US/11/072,512
 CURRENT FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US 60/350,978
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: JP 2001-379298
 PRIOR FILING DATE: 2001-11-05
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2798
 LENGTH: 391
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-072-512-2798

Query Match 63.0% Score 1272; DB 11; Length 391;
 Best Local Similarity 62.0%; Pred. No. 1.7e-113; Gaps 2;
 Matches 232; Conservative 58; Mismatches 68; Indels 16;

Qy 20 EASTCRSSRPCSGS-----MWSSE--SKRTLTSLSWALQPEVITQOYLSSGM 63
 Db 14 ETIDCRNTRTCGSKPSQPTSPHADRWNHFRKQDLDNIVTPETVQLYNGGL 73
 Qy 64 CGYDLDGGPVWVDIIGPKDAKGILFSASQDLIRTKNRECECELLQECAHQYTKLGRKVET 123
 Db 74 CGYDYEQQPVYFNITGSDPKGILLSSAKQDNTRKRTKVCCELLHECELQTKLGRKITEM 133
 Qy 124 ITTYDCSGLGLKHLWKAEEVAGEFLCMFENNPETLKLRLVPAKLPFPAANLJKPF 183
 Db 134 ALLVFDMEGLSLKHLWKAEEVYQQFFSILEANYPETLKLNLIVTRAPKLPFPAANLVKSF 193
 Qy 184 LSEDTRKHMVLGSAKYKEVLLKHSIDPQDVPEYGGMTDIDPQDNPKCKSKINNGGDIPRKY 243
 Db 194 MSEETRKKIVLQDNLKELTRISPDLVPEGGMIDPQDNPKCKSKINNGGDIPRKY 253
 Qy 244 YRDQVKQQYEHSYQISRGSSHOVEYEILFPGCCLWCMFMSDGADYGFIFLKTKMGERQ 303
 Db 254 YLCBQVRQLEHTRSVRGSSLOVENEILFPGCVRMFAQASDDGGDGFGLKTMGEQ 313

Db 241 YGGTMTDDGPKCKSKINYGGDI PRKXYVRDQVKQQYEHSYQISRGSSHOVEYEILFPG 300
 Qy 304 RAGENTEVLPNQRYNSHLVPEDTLTCSDPGIYVURFDNTYSFTHAKKVNFTVEVLLPDK 363
 Db 314 SARENTEVLPNQRYNSHLVPEDTLTCSDPGILCQAGVYVRFDNTYSRMKRSYTVEVLLPDK 373
 Qy 364 ASEEKMKQLGAGTP 377
 Db 374 ASEETQSLXAMRP 387

RESULT 3

US-11-072-512-3609
 ; Sequence 3609, Application US/11072512
 ; Publication No. US20060029945A1
 GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: SATO, HIROTOKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUKIKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOKIKO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOKI
 ; APPLICANT: NAGABARI, KENJI
 ; APPLICANT: MASUBO, YASUHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: 084335-0191
 CURRENT APPLICATION NUMBER: US/11/072,512
 CURRENT FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US 60/350,978
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: JP 2001-379298
 PRIOR FILING DATE: 2001-11-05
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3609
 LENGTH: 360
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-072-512-3609

Query Match 55.4% Score 1118; DB 11; Length 360;
 Best Local Similarity 66.1%; Pred. No. 7.9e-99; Mismatches 52; Indels 0; Gaps 0;
 Matches 197; Conservative 49; Mismatches 52; Indels 0; Gaps 0;

Qy 40 KRTLTSLSLWALQPEVITQOYLSSGMCGYDLCGCPWVYDIIGPKDAKGILFSASKQDLIRTK 99
 Db 11 QQDLNIVTWWQPEVITQOYLSSGMCGYDLCGCPWVYDIIGPKDAKGILFSASKQDLIRTKR 70
 Qy 100 MRECELLQECAHQYTKLGRKVETTLYDEGLGLGHHLWKPAYEFLCMFENNPET 159
 Db 71 IKVCELLIHECELOTQKLGRKITEMALMFDMEGLSLKHLWKPAYEYQQFFSILEANPY 130
 Qy 160 TLKRLFVVKAPKLFPVAYNIJKPFLSEDTRKIMVLGANYKEVLLKHSIDPQDVPEYGGT 219
 Db 131 TLKRLFVVKAPKLFPAFLNVLKFSEBTRKIVIJDNWQELTFPISPOLVPEFGGT 190
 Qy 220 MTDPGNPKCKSKINNGGDI PRKYYVRDQVKQQYEHSYQISRGSSHOVEYEILFPGCCLW 279
 Db 191 MTDPGNPKCKSKINNGGDI PRKYYVRDQVKQQYEHSYQISRGSSHOVEYEILFPGCCLW 250
 Qy 280 WOFMSDCAEVGFIFLKTKMGERQZGEMTEVLPHORYNSHLVPEGTITCSDPGIYV 337
 Db 251 WQFASDGGDIFGFVFLKTMGEQOSAREMTEVLPQSYRNAHMVPEDGSLTCLQAGYVY 308

RESULT 4
 US-11-096-568A-7798
 ; Sequence '798, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO: 7798
 ; LENGTH: 463
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1) ..(463)
 ; OTHER INFORMATION: Ceres Seq. ID no. 15175774
 US-11-096-568A-7798

Query Match 11.5%; Score 233; DB 11; Length 463;
 Best Local Similarity 27.1%; Pred. No. 4.9e-14;
 Matches 71; Conservative 40; Mismatches 113; Indels 38; Gaps 5;

Qy 34 MWSESEK-----RTLTLSLAWQPPEVQQYLGGMCGYDLDGCPWYDIIGPKDAKGL 86
 Db 89 MWSEMLKWRKEFGADTTIDFLEKELDEVQYPGHGVDKDGRPYTIERLGQVDAKTM 148

Qy 87 LFSASKQDLRTRKRECE---LLQECAHQTTKLRKVETITIYDCEGLKLHWKPA 142
 Db 149 MQVTMDRYIKHKEFERTFDVKFAACSTAARK--HIDQSTTILDVGVLKSFSKHA 205

Qy 143 VEAYGEFLCMFEENYPETKLRLFVVKAPKLFPVAVNLKPFELSEDTRKIMVLGANYKEV 202
 Db 206 RELVTRLQKDGDNYPETLNRMFINAGSGFRILWNTVRSFLDPKTTAKINVGNKYDTK 265

Qy 203 LLKHISPDQPVPEYGGMTDPD-----GNPKCKSKINYGGDI 239
 Db 266 LLEIIDASELPFLGGCTCAOGCGRSDKGPMKDAEVYMRMVQNGDHKCSRSASQGEE 325

Qy 240 PRKYVYRDQV-KOQYEHVSQIS 260
 Db 326 EKENSEEHKTSKLEANHTPQLS 347

RESULT 6

US-11-096-568A-7796

; Sequence 7796, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO: 7796
 ; LENGTH: 483
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1) ..(483)
 ; OTHER INFORMATION: Ceres Seq. ID no. 15175772
 US-11-096-568A-7796

Query Match 11.5%; Score 233; DB 11; Length 483;
 Best Local Similarity 27.1%; Pred. No. 4.9e-14;
 Matches 71; Conservative 40; Mismatches 113; Indels 38; Gaps 5;

Qy 34 MWSESEK-----RTLTLSLAWQPPEVQQYLGGMCGYDLDGCPWYDIIGPKDAKGL 86
 Db 93 MWSEMLKWRKEFGADTTIDFLEKELDEVQYPGHGVDKDGRPYTIERLGQVDAKTM 152

Qy 87 LFSASKQDLRTRKRECE---LLQECAHQTTKLRKVETITIYDCEGLKLHWKPA 142
 Db 153 MQVTMDRYIKHKEFERTFDVKFAACSTAARK--HIDQSTTILDVGVLKSF SKHA 209

Qy 143 VEAYGEFLCMFEENYPETKLRLFVVKAPKLFPVAVNLKPFELSEDTRKIMVLGANYKEV 202
 Db 210 RELVTRLQKDGDNYPETLNRMFINAGSGFRILWNTVRSFLDPKTTAKINVGNKYDTK 269

Qy 203 LLKHISPDQPVPEYGGMTDPD-----GNPKCKSKINYGGDI 239
 Db 270 LLEIIDASELPFLGGCTCAOGCGRSDKGPMKDAEVYMRMVQNGDHKCSRSASQGEE 329

Qy 240 PRKYVYRDQV-KOQYEHVSQIS 260
 Db 330 EKENSEEHKTSKLEANHTPQLS 351

RESULT 7

US-11-096-568A-28170
 ; Sequence 28170, Application US/11096568A
 ; Publication No. US20060048240A1

Query Match 11.5%; Score 233; DB 11; Length 479;
 Best Local Similarity 27.1%; Pred. No. 4.9e-14;
 Matches 71; Conservative 40; Mismatches 113; Indels 38; Gaps 5;

Qy 143 VEAYGEFLCMFEENYPETKLRLFVVKAPKLFPVAVNLKPFELSEDTRKIMVLGANYKEV 202

Db 210 RELVTRLQKDGDNYPETLNRMFINAGSGFRILWNTVRSFLDPKTTAKINVGNKYDTK 269

Qy 203 LLKHISPDQPVPEYGGMTDPD-----GNPKCKSKINYGGDI 239

Db 270 LLEIIDASELPFLGGCTCAOGCGRSDKGPMKDAEVYMRMVQNGDHKCSRSASQGEE 329

Qy 240 PRKYVYRDQV-KOQYEHVSQIS 260

Db 330 EKENSEEHKTSKLEANHTPQLS 351

GENERAL INFORMATION
 APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO: 28170
 LENGTH: 478
 TYPE: PRT
 ORGANISM: *Arabidopsis thaliana*
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Ceres Seq. ID no. 2705654
 US-11-096-568A-28170

Query Match 11.0%; Score 221.5; DB 11; Length 478;
 Best Local Similarity 26.8%; Pred. No. 6.1e-13; Indels 31; Gaps 6;
 Matches 70; Conservative 44; Mismatches 116; Del/Ins 31; Gap 6;

Qy 31 SGGMWSSSK-----RLTTSLAWQPPEVQQYLSSGMCYDLDCCPWWYDIIGPKDA 83
 Db 16 TNQMWSDMLRWRKEFQDVTMEDREFKIDEVLKYPPQGHICRGRPVYTERLCQVDS 75

Qy 84 KGLLFSASKQDLIRTRRECE---LLIQCAHOTTKLGRKVETITIYDEBGLKHLW 139
 Db 76 TKLMQVTTMDRYVNYHMEFERTENKFPCASIAKK--HIDQSSTILDVQGVGLKFN 132

Qy 140 KPAVEAYGEFLCMFEENYPETUKRLFVVKAPKLFPVAYNLKPFLESDTRKKIMVLGANY 199
 Db 133 KAARDLITRLQVDGDNTPETINRMFLINAGSGFMRMINTVSKFLDPKTTAKIHLGNKY 192

Qy 200 KEVLKHISPDQPVYEGGTTMT-----DPDGNPCKSKLKNYGGDIPRKYVYRD 247
 Db 193 QSKLELTIDASLPFLGGSCCADNGCMRSDKGPNNNPDIMKRVNNGDHICSK--RS 249

Qy 248 QVKQYEHSVQISRGSSHQVE 268
 Db 250 QADNAGENI--ISQGNNNSAVE 268

RESULT 8
 US-11-096-568A-28169
 Sequence 28169, Application US/11096568A
 Publication No. US20060048240A1

GENERAL INFORMATION
 APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO: 28169
 LENGTH: 517
 TYPE: PRT
 ORGANISM: *Arabidopsis thaliana*
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)-(517)
 OTHER INFORMATION: Ceres Seq. ID no. 2705653
 US-11-096-568A-28169

Query Match 11.0%; Score 221.5; DB 11; Length 517;
 Best Local Similarity 26.8%; Pred. No. 6.8e-13; Indels 31; Gaps 6;
 Matches 70; Conservative 44; Mismatches 116; Del/Ins 31; Gap 6;

Qy 31 SGGMWSSSK-----RLTTSLAWQPPEVQQYLSSGMCYDLDCCPWWYDIIGPKDA 83
 Db 55 TNQMWSDMLRWRKEFQDVTMEDREFKIDEVLKYPPQGHICRGRPVYTERLCQVDS 114

RESULT 9
 US-11-096-568A-28168
 Sequence 28168, Application US/11096568A
 Publication No. US20060048240A1

GENERAL INFORMATION
 APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO: 28168
 LENGTH: 558
 TYPE: PRT
 ORGANISM: *Arabidopsis thaliana*
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)-(558)
 OTHER INFORMATION: Ceres Seq. ID no. 2705652
 US-11-096-568A-28168

Query Match 11.0%; Score 221.5; DB 11; Length 558;
 Best Local Similarity 26.8%; Pred. No. 7.6e-13; Indels 31; Gaps 6;
 Matches 70; Conservative 44; Mismatches 116; Del/Ins 31; Gap 6;

Qy 31 SGSMWSSSK-----RTLTTSLAWQPPEVQQYLSSGMCYDLDCCPWWYDIIGPKDA 83
 Db 96 TNQMWSDMLRWRKEFQDVTMEDREFKIDEVLKYPPQGHICRGRPVYTERLGVDY 155

Qy 84 KGLLFSASKQDLIRTRRECE---LLIQCAHOTTKLGRKVETITIYDEBGLKHLW 139
 Db 156 TKLMQVTTMDRYVNYHMEFERTENKFPCASIAKK--HIDQSSTILDVQGVGLKFN 212

Qy 140 KPAVEAYGEFLCMFEENYPETUKRLFVVKAPKLFPVAYNLKPFLESDTRKKIMVLGANY 199
 Db 213 KAARDLITRLQVDGDNTPETINRMFLINAGSGFMRMINTVSKFLDPKTTAKIHLGNKY 272

Qy 200 KEVLKHISPDQPVYEGGTTMT-----DPDGNPCKSKLKNYGGDIPRKYVYRD 247
 Db 273 QSKLELTIDASLPFLGGSCCADNGCMRSDKGPNNNPDIMKRVNNGDHICSK--RS 329

Qy 248 QVKQYEHSVQISRGSSHQVE 268
 Db 330 QADNAGENI--ISQGNNNSAVE 348

RESULT 10
 US-11-096-568A-32080
 Sequence 32080, Application US/11096568A
 Publication No. US20060048240A1

GENERAL INFORMATION
 APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO: 32080
 LENGTH: 409
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(409)
 OTHER INFORMATION: Ceres Seq. ID no. 13592122
 US-11-096-568A-32080

Query Match Score 10.7%; Pred. No. 1.6e-12; Mismatches 139; Indels 132; Gaps 17; Best Local Similarity 94%; Conservative 58; Mismatches 139; Indels 132; Gaps 17; Matches 94; Conservative 58; Mismatches 139; Indels 132; Gaps 17;

Qy 5 VGDLSPROKEAL-AKPEASTCRSRPCSGMS-
 Db 65 VSPLEKPTQKSIOELKEKLASSSK--ASSWNCVSLIGGGDDKADVILKFLRARDFKVA 121
 Qy 38 ESKRTLTTSLAWQPPEVQQY-----LSSG---MCGYDLDGCPWYDIIG---PKD 82
 Db 122 DSURMLKECLWEEFKAELTEEDLGFKDLEGKVAYARGYDKEGHPVVCNAYGVFKEKE 181
 Qy 83 AKGLLFPSASKO--DLIIRTQMRECELLLOECAHQTTLGRK-----VETITIYDCEG 132
 Db 182 MYERVGDKBEKLINKFLRWRV-----QVLERGYKMLHFKPGGVNSIIQVTDLKD 229
 Qy 133 LGKHLWKPAVEAYGEFLCMFEENYPETKLRLFVVKAPKLFPVAYNLIKPFLSEDTRKK- 191
 Db 210 MPKREL---RVSNQULSLFQDNQYPLVATKTFINPVFSVYMSFSPFLQTQTSKF 285
 Qy 192 IMVLGANYKEVLKHKISPDQPVYSGMTDPD---GNPKCKSKINYYGGDIPRKYYVRDQ 248
 Db 286 VMSKEGNAETLNMKFRPEDIQYGLSRPRTDSQNPPXPASEFSIKG----- 334
 Qy 249 VKQQYEHSVQISRGSSHOVEYLFPGCVLRWMQMSDGAvgFGFLKTMGERORAGEM 308
 Db 335 -----GEKVNQIEGEGATITWDIVVGGNDLEYs----- 365
 Qy 309 TEVLPNQRYNSHLVPED-----GTLICSDPGIVYLRFDNNTYSF1HAKV-----N 353
 Db 366 AEFVPNAESEYAVWEKPKKMKATDEAVCNSFTTVEAGKLILSVDTTLS-RKVKVAAZR 423
 Qy 354 FTV 356
 Db 424 YTV 426

RESULT 1.2
 US-11-096-568A-27441
 ; Sequence 27441, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO: 27441
 ; LENGTH: 511
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(511)
 ; OTHER INFORMATION: Ceres Seq. ID no. 1815699
 US-11-096-568A-27441

Query Match Score 10.6%; Pred. No. 3.5e-12; Mismatches 35; Indels 14; Gaps 3; Best Local Similarity 28.7%; Conservative 35; Mismatches 95; Indels 14; Gaps 3;

Qy 34 MWSSS-----SKRTLTSLAWQPPEVQQYLSGGMCGYDLDGCPWYDIIGPKDAKGL 86
 Db 57 MWSMDIQWRKDGFADTIEDDFEEDEVNKHYPOQYHGTDKEGRVVYIERGQIDANKL 116
 Qy 87 LFSASQDLIIRTQKRECE---LLIQCQCAHQTTLGRKVTITIYDCEGLGLKHJMKPA 142
 Db 117 LQTTMDRYTKVHYKEFEKTFKVPPCSVYANK--HIDOSTTILDVQGVGLKRNFSKSA 173
 Qy 143 VEAGFLCMFEENYPETKLRLFVVKAPKLFPVAYNLIKPFLSEDTRKKMIVLGAJYKEV 202
 Db 174 REJLRLCKDNEENYPETLNRMFINAGSGPRLMSTVKSPLDPKTAKIHVLGNYCHSK 233
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO: 13592122
 ; TITLE OF INVENTION: Therby
 ; FILE REFERENCE: 2750-1592PUS2
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(433)
 ; OTHER INFORMATION: Ceres Seq. ID no. 13592122
 US-11-096-568A-32079

RESULT 13
 US-11-096-568A-27440
 Publication No. US/11/096568A
 GENERAL INFORMATION:
 APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Therry
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 27440
 LENGTH: 551
 TYPE: PRT
 ORGANISM: *Arabidopsis thaliana*
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1) ..(551)
 OTHER INFORMATION: Ceres Seq. ID no. 1815698
 US-11-096-568A-27440
 Query Match Score 214; DB 11; Length 551;
 Best Local Similarity 28.7%; Pred. No. 3..9e-12;
 Matches 58; Conservative 35; Mismatches 95; Indels 14; Gaps 3;
 Qy 34 WSSE----SKRTLTSLAWQPETKLFLVKAPEKLYVQYDGGCPWYDIDGPKDAKGL 86
 Db 97 MWSDMIQWRKDFGADTIEDDEFEEDEVMKHYPOGYHVDKEGRPYTERGQIDANKL 156
 Qy 87 LFSASKDQLRTKMRCE---LLQEGAHOTTKLGRVETITIYDCEGLGLKHLWKA 142
 Db 157 LQVTMDYVKYVKEFETKLFLVKAPEKLYVQYDGGCPWYDIDGPKDAKGL 86
 Qy 143 VEAYGEFLCMFEENYPETKLFLVKAPEKLYVQYDGGCPWYDIDGPKDAKGL 86
 Db 214 REJJQRICKDNENYPETLNRMFINAGSFRLLWSTVKSFLDPKTTAKIHLGNKCHSK 273
 Qy 203 LLKHISPPQVPEYGGTMIDPD 224
 Db 274 LLEVIDASELPFFGGACTCED 295
 RESULT 14
 US-11-096-568A-27439
 Publication No. US/11/096568A
 GENERAL INFORMATION:
 APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Therry
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 27439
 LENGTH: 560
 TYPE: PRT
 ORGANISM: *Arabidopsis thaliana*
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1) ..(560)
 OTHER INFORMATION: Ceres Seq. ID no. 1815697
 Query Match Score 214; DB 11; Length 560;
 Best Local Similarity 28.7%; Pred. No. 4e-12;

Matched 58; Conservative 35; Mismatches 95; Indels 14; Gaps 3;
 Qy 34 WSSE----SKRTLTSLAWQPETKLFLVKAPEKLYVQYDGGCPWYDIDGPKDAKGL 86
 Db 106 MWSDMIQWRKDFGADTIEDDEFEEDEVMKHYPOGYHVDKEGRPYTERGQIDANKL 165
 Qy 87 LFSASKDQLRTKMRCE---LLQEGAHOTTKLGRVETITIYDCEGLGLKHLWKA 142
 Db 166 LQVTMDYVKYVKEFETKLFLVKAPEKLYVQYDGGCPWYDIDGPKDAKGL 222
 Qy 143 VEAYGEFLCMFEENYPETKLFLVKAPEKLYVQYDGGCPWYDIDGPKDAKGL 86
 Db 223 REJJQRICKDNENYPETLNRMFINAGSFRLLWSTVKSFLDPKTTAKIHLGNKCHSK 282
 Qy 203 LLKHISPPQVPEYGGTMIDPD 224
 Db 283 LLEVIDASELPFFGGACTCED 304
 RESULT 15
 US-11-096-568A-9415
 Sequence 9415, Application US/11/096568A
 Publication No. US/2006/0048240A1
 GENERAL INFORMATION:
 APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Therry
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 9415
 LENGTH: 394
 TYPE: PRT
 ORGANISM: *Triticum aestivum*
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) ..(394)
 OTHER INFORMATION: Ceres Seq. ID no. 12460984
 US-11-096-568A-9415
 Query Match Score 213; DB 11; Length 394;
 Best Local Similarity 24.9%; Pred. No. 3e-12;
 Matches 80; Conservative 46; Mismatches 147; Indels 48; Gaps 10;
 Qy 35 WSSE--SKRTLTSLAWQPETKLFLVKAPEKLYVQYDGGCPWYDIDG---PKDAGLILFS 89
 Db 95 WRAEFRADAVLDLGPKDLEGIVAY---MGWDRDGHPYCYNAGVFKORDMYDRVFG 150
 Qy 90 ASQDQLLRTKMRCECLLQECAHOTTKLGRVETITIYDCEGLGLKHLWKAPEAVEAYGEF 149
 Db 151 DS--DRUSRFLWRVQIMERGVRLQLRPGGYNATQVTLKMPKREL---RAASNQI 204
 Qy 150 LCMFEENYPETKLFLVKAPEKLYVQYDGGCPWYDIDG---PKDAGLILFS 89
 Db 205 LSFLFDQNPYKMPVARYFVNVPYFYSVLSMISPFLTRTSKVFIREGVNTAELFKIR 264
 Qy 209 PDOPVVEYGGTMIDPD---GNPKCKSKINYGDIIPRKYYDQVQQYEHSVQISRGSSH 265
 Db 265 PELPVQYGGLSRASELENGPKPASEFTIKG-----GEKV 300
 Qy 266 QVEYEILFPGCVLRWQFMSDGADEVGF1-FLKTIGERQRAGEMTEVLPNQRYNSHLYPE 324
 Db 301 FLRIDGEAGATITWDLVGGWLEIGAEYVPASEGTYLCVERTKVPAADE---PV 356
 Qy 325 DGTLLTCSDPGIVYLRFDTNYS 345
 Db 357 HNAFTAKEPGKVNLSIDNSGS 377
 Search completed: May 2, 2006, 18:53:58
 Job time : 28 secs

RESULT 2		
A53057	retinal-binding protein - Japanese flying Squid	
C.Species: Todarodes pacificus (Japanese flying Squid)		
C.Accession: A53057	DB: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004	
R.Ozaki, K. Terada, A.; Ozaki, M.; Hara, R.; Hara, T.; Hara-Nishimura, I.; Mori, H.; J. Biol. Chem. 269, 3838-3845, 1994		
A.Title: Molecular characterization and functional expression of squid retinal-binding protein		
A.Reference number: A53057; PMID:94148895; PMID:8106428		
A:Accession: A53057		
A.Status: preliminary		
A:Molecule type: mRNA; Protein		
A:Residues: 1-343 <OZ2>		
A:Cross-references: UNIPROT:P49193; UNIPARC:UPI000016C018; GB:S68871; NID:9545382; PID:9		
A:Experimental source: eye		
A:Note: sequence extracted from NCBI backbone (NCBIN:143812, NCBIPI:143813)		
Query Match 32.8%; Score 661.5; DB 2; Length 343;		
Best Local Similarity 37.2%; Pred. No. 2.2e-48;		
Matches 122; Conservative 82; Mismatches 115; Indels 9; Gaps 2;		
Qy 49 WQPPEVIOQYLSGGMCYDLDGCPWVYDIIGPKDAKGILFSASKQDLRLRTKMRRECELLQ 108	RESULT 4	
Db 16 YTPPDVIRKEMTGVDGDKGSLVRLEPVGIDMKGIMYSCKRSDEIKSKULLQCEERHLK 75	S28303	
Qy 109 ECAHQTTLGRKVETITIYDCBGLKHLMKPAAVEAYGEFLCMFEENYPETKLRFVKK 168	hypothetical protein T23G5.2 - Caenorhabditis elegans	
Db 76 DLEAQSERVKPKCTGTVDFMENVSGHMMRKGGLDMNLYLQVLEDNPYPERMKRULFVIN 135	C.Species: Caenorhabditis elegans	
Qy 169 APKLFPVAYNLKPLPSDTRKIMVILGANYKEVLKHISPVQVPAVEAYGEFLCMFEENYPETKLRFVKK 228	C.Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004	
Db 136 APLTFPVLYKVKPLSSDMKMKIFVLGDKYDFTLLEVIDABELPAYGTTKS - EGDEK 193	C;Accession: S28303	
Qy 229 CKSKINYGDIPKRYYDQVKQYEVHSVQISRGSSHQVEYLIFPGCVLRQFMDSGAD 288	R;Berks, M.	
Db 194 CSELIICHGEVPGEFLNTDDPETMETITVSGDKYVEELENENTYIKWEYKTEHD 253	Submitted to the EMBL Data Library, December 1992	
Qy 289 VGRGIFPLTKMGERQRAGEMTEVLPNQRYNSHLVPEPDGTLCSDPGIYVLRFDNTYSFH 348	A;Reference number: S28296	
Db 254 IGROLF-----RKGNDWEEVYPTIERTDCSMTLQSHKCRDGTIALCFDNFSMMT 306	A;Accession: S28303	
Qy 349 AKRNFTTEVLLDKASERBMQLGAGT 376	A;Molecule type: DNA	
Db 307 SKRVRYTAEVMDDEVSDSNDNMKIDST 334	A;Cross-references: UNIPROT:Q03606; UNIPARC:UPI000017BB0; EMBL:219158	
Qy 49 WQPPEVIOQYLSGGMCYDLDGCPWVYDIIGPKDAKGILFSASKQDLRLRTKMRRECELLQ 108	A;Introns: F;32-240/Domain: cellular retinaldehyde-binding protein homology <CRB>	
Db 68 WTRPTVTKQYFPGWINSKAGRPMYTLRFGOLDKMLRSGVENIVKLTLUSICEDGLQ 127	A;Length: 470;	
Qy 109 ECAHQTTLGRKVETITIYDCBGLKHLMKPAAVEAYGEFLCMFEENYPETKLRFVKK 168	Score 388.5; DB 2; Length 470;	
Db 128 RAAEATRKLGKTPISWSNLVVDGLGSMRHLWRPGQCLLKIEIVEANYPETMGQVLVRR 187	Best Local Similarity 28.2%; Pred. No. 5.3e-25;	
Qy 169 APKLFPVAYNLKPLPSDTRKIMV--LGANYKEVLKHISPVQVPAVEAYGEFLCMFEENYPETKLRFVKK 225	Mismatches 136; Indels 75; Gaps 10;	
Db 188 APRVPPFLWTLISPDEKTRKKFMYGSGSCDLDKELRKBEKIPDFEGGS-C---- 242		
Qy 226 NPCKSKINYGGDIPRCKYVRDQVKQYEVHSVQISRGSSHQVEYEILFP--- 274		
Db 243 ---LTINCGLGLGSHVPKMSYL--PVEEDEGASSSEDPLHSTYSTATWRGPYEVVIRLET 297		
Qy 275 -GCULRQEMSDGADYFGIYFLKTKQE --RQAGEMTEVU----- 316		
Db 298 AGCVALMDFDVLLKNDCEFSLYSTEKEQPAVRDGAQSPTTILNPVEMVSAAIGGASHQH 357		
RESULT 3		
T23057	hypothetical protein H06001.3 - Caenorhabditis elegans	
C.Species: Caenorhabditis elegans		
C.Accession: T23057	DB: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004	
R.Barlow, K.		
Submitted to the EMBL Data Library, March 1997		
A:Reference number: Z19665		
A:Accession: T23057		
A:Status: preliminary; translated from GB/EMBL/DDBJ		
A:Molecule type: DNA		
A:Residues: 1-383 <WIL2		
A:Cross-references: UNIPROT:O17007; UNIPARC:UPI0000078A7E; EMBL:252970; PIDN: CAB07482.1;		
C.Genetics:		
A:Gene: CESPH06001.3		
A:Map Position: 1		
A:Introns: 21/2; 75/3; 137/3; 190/2; 219/3; 302/2; 358/1		
Query Match 20.2%; Score 408; DB 2; Length 383;		
Best Local Similarity 29.6%; Pred. No. 8.9e-27; Mismatches 142; Indels 8; Gaps 7;		
Matches 93; Conservative 71; Mismatches 142; Indels 8; Gaps 7;		
Qy 345 SP-IHAKKVNFTVEVL 359		
Db 418 DFGSHKCRLLIYVIL 433		

RESULT 5

B88551 Protein T23G5.2 [Imported] - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: B88551
 R;Anonymous: The *C. elegans* Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A;Reference number: A75000; MUNDI:9009613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A;Accession: B88551
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-743 <STO>
 A;Cross-references: UNIPROT:Q03606; UNIPARC:UPI000013BA54; GB:chr_III; PIDN:CAA79573.1;
 C;Genetics:
 A;Gene: T23G5.2
 A;Map position: 3

Query Match 19.3%; Score 388.5; DB 2; Length 743;
 Best Local Similarity 28.2%; Pred. No. 9.9e-25; Mismatches 59; Indels 10;
 Matches 106; Conservative 59; Mismatches 136; Gaps 10;

Qy 49 WQPPEVQIQLGSGMCGIDGCPWYDIDGPKDAKGILFASAKDLRTRKRECELLQ 108
 Db 341 WTRPRTVKQYFPGWHNSDKAGREMYLIRFGOLDTKGMRSCGVENLYKLTLSICEDLQ 400

Qy 109 ECAHOTTKLRGRKVETITIYDCEGGHLKHWKPAVEAYEFLCMFEENYPETKLRLFVVK 168
 Db 401 RAAEAATRKUGTPISSWSLVLDDGSMRHLWPGVQCLIKIIIVEANYPETKGQLVVR 460

Qy 169 APKLPVVAYNLKPKFLSEDTRKKLIMV--LGANVKEVLKHKISPDQVPEYGTTMTDPDG 225
 Db 461 APRVFPVLMPLISPIDEXTRKCKMVGSSGGDLIKELRKHIERKFPIPDFLGSSC---- 515

Qy 226 NPCKSKINNGGIDPRKYVTRDQVKQQYE-----HSVQISRGSSHSSHOVEYLFP--- 274
 Db 516 --LTTCNGLGGHPKSMYL--PVEEQGASSSEDPHISTYTSPATWGPYEVVPILET 570

Qy 275 -GCYLRWQFMDSGADYFGFLKTNGE---RORAGENTEVL-----PNQR 316
 Db 571 AGCVETWDFTDVLRNDCFSLYSTEKIEPAVRDGAQSPTTINPVENSAAGGASHOH 630

Qy 317 YNSHLVPE-----DGTLTCSDPGIVYIILF-----DNTRY 344
 Db 631 PDLQCAPELKIGTPQLRLEEKAVYFQEGDSMOGHYSCHSRA GTYIMQNRVPETAA GHSSTF 690

Qy 345 SF-THAKKNFTVEVL 359
 Db 691 DFGSHHKCRLLYYEIL 706

RESULT 6

T24897 hypothetical protein T13H5.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T24897
 R;Lightning, J.
 Submitted to the EMBL Data Library, October 1995
 A;Reference number: Z19950
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1254 <WIL>
 A;Cross-references: UNIPROT:Q22467; UNIPARC:UPI000017BBA2; PIDN:CAA91418.1;
 C;Genetics:
 A;Gene: CESP:T13H5.2

A;Map position: 2; Score 286/2; 404/3; 437/1; 539/3; 616/1; 688/3; 732/3; 778/3; f
 A;Introns: 63/1; 158/2; 200/3; 286/2; 404/3; 437/1; 539/3; 616/1; 688/3; 732/3; 778/3; f

Query Match 16.6%; Score 334; DB 2; Length 1254;
 Best Local Similarity 27.2%; Pred. No. 8.6e-20; Mismatches 91; Conservative 144; Indels 26; Gaps 9;

Qy 57 QYLSGMCGYDLDGCPWYDIDGPKDAKGILFASAKDLRTRKRECELLQECAHQTTK 116
 Db 104 RYLPGLSLGIDHENNYVSLQMIIGHDAGLMPATRNSDLYMRAESBGVMQIRKMEKE 163

Qy 117 LGRKVETITIYDCEGIGLKLWKPAVEAYEFLCMFBNENYETKLRFVVKAPKLFPEVA 176
 Db 164 QGPKLGT-SVIFDGLGMSMQVIDLALKVVTMLSQLOEMFPDVIRKIFIVNTPTFQVL 222

Qy 177 YNLIKPFLSEDTRKKLIMVLAGNYKEVLKHKISPDQVPEYGTMTDDGPNPKKSINY- 235
 Db 223 WSMISPCLAKOTQQKVTKLGNWDQHJKRNGTGBEVLPBRWGSTR-----KAETBYG 273

Qy 236 ----GGD1PR--KYVYRDQKQOQYEHSVQISRGSSH--QVEYELFLFGQCVLRWFQMSDGA 287
 Db 274 NVRMGGKVPAAELKVDANDLPALKTLYKLNVSARSTTEVPTILEGVNPGRKLWYWMLRENN 333

Qy 288 DVGFQIFILRKTMGKBRQAGEMPE--VLPQNQRVNSHLYPEDGTLCSDPGIVYIYLRFDNTYS 345
 Db 334 DINFSI-LRAAESEKVOAHHDDMMVHPKPKLQTDVFPEDEGCIAAEPGVYKVFEDNTHS 392

Qy 346 FTHAKKNFTVEVLIPDKASEEKKK---QLGAGTP 377
 Db 393 KLRKTVKXIFI-RMSLCETERSKTNNGNCIP 426

RESULT 7

A96745 probable cytosolic factor T9N14.8 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A96745
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso-Chin, C.W.; Chang, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lurop, J.S.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; PMID:21016719;
 C;Genetics:
 A;Map position: 1
 A;Molecule type: DNA
 A;Residues: 1-490 <STO>
 A;Cross-references: UNIPROT:Q9C7T9; UNIPARC:UPI00009C593; GB:AB005173; NID:910645378;

Qy	197 -ANYKEVILKHSISPDQVPEYGGTMTDP-DGNPKCKSKINYGGDIPRKYYVRDVQKQYE 254	A;Accession: T38768 A;Status: preliminary; translated from GB/EMBL/DBBJ
Db	349 PSRSAETLFKYISPEQEVQYGLSVDPDCNP-----DFSLEDSASE--- 391	A;Molecule type: DNA A;Residues: 1-286 <GEN>
Qy	255 HSVQIISRSRSHOYEIEIFPGCVLWRQWOMSDGADGFGIFLKTKMGERQRAGEMTEVLNP 314	A;Cross-references: UNIPROT:Q10137; UNIPARC:UPI00001355BA; EMBL:Z69086; PTDN:CAA93167.1.
Db	392 --ITVKPCTKQVEI-IYEKCELVWEIRVGMEVS----- 424	A;Experimental source: strain 972h-; cosmid C3H8
Qy	315 QRYNSHLVPEDG--TLCSDPQIYVILRFDTNTYSFHAKKYNFTVEYLPLDKASEEKKMKQ 371	C;Genetics:
Db	425 --YKAEPFPEEKDAYVVIQKP-RKMRPSDEPVLTFSKVNLGKVLTVDNPTSKKK 480	A;Gene: SPAC3H8.10 A;Map position: 1 A;Intron: 53/3; 154/3; 195/3 C;Superfamily: cellular retinaldehyde-binding protein homology <CRB> Db 481 L 372
Qy	372 L 372	Query Match 11.3%; Score 228; DB 2; Length 286;
Db	481 L 481	Best Local Similarity 31.3%; Pred. No. 1.e-11; Mismatches 84; Indels 4; Gaps 3; Matches 59; Conservative 38;
RESULT 8		
Qy	CG6329 hypothetical protein F14P1.2 [Imported] - Arabidopsis thaliana	Qy 43 LTTSLAWQPPEVIOQYLGGMCYDLDGCPWPYD1GPKDAKGLLFSASKODLLRTKMR 102 Db 86 LIKNFHYDEKEAVSKYPOFYHTKTDIDGRPYVEQLGNIDLKLQYQITTPERMQMLVYE 145
Db	hypothetical protein F14P1.2 [Imported] - Arabidopsis thaliana (mouse-ear cross)	Qy 103 CELLL-LQECAHOTTKLGRKVETITTYDC8GLGLKHLWPKAVEAY-GEFLCMFEENYPET 160 Db 146 YEMMLAKRPFACSRKAGGLTSCTIMDLKVGIVTSI-HSVDYSTROASSISQDYPER 203
Qy	C;Species: Arabidopsis thaliana (mouse-ear cross)	Qy 161 LKRLFIVVKAPLKFVPPAVYLNLPKFLSEDTRKIMVILGANVYKEVLKHLISPDQVPEYGGTM 220 Db 204 MGKFVYVINAQPGFSSAFNLKGFLLDEATVRKIHLSNYKSALLEQIPADNLPAKUGGNC 263
Db	C;Accession: C86329 #Sequence_revision 02-Mar-2001 #text_change 09-Jul-2004	Qy 221 TDPDG 225 Db 264 QCPGG 268
RESULT 10		
Qy	RTheologis, A.; Ecker, J. R.; Palm, C. J.; Federspiel, N. A.; Kaul, S.; White, O.; Alonso, C.; Chung, M. K.; Conn, L.; Conway, A. R.; Creasy, T. H.; Dewar, K.; aranen, N. D.; Hughes, E.; Huizar, L.	Qy 291 761-768. 1999 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffit, K.; Cronin, L.A.; Vanaken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Db	Nature 408, 816-820, 2000	A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A86141; PMID:21016719; PMID:11130712
Qy	A;Accession: C86329 #Sequence_revision 02-Mar-2001 #text_change 09-Jul-2004	A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A86141; PMID:21016719; PMID:11130712
Db	A;Status: preliminary	C;Species: Arabidopsis thaliana (mouse-ear cross)
Qy	A;Molecule type: DNA	C;Accession: C84561 #Sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
Db	A;Residues: 1-457 <STR>	R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Qy	A;Cross-references: UNIPROT:Q9FWR9; UNIPARC:UPI00000A4BF4; GB:AE0005172; NID:g9795590; PI	C;Genetics: C84561 C;Accession: C84561 A;Map position: 1
Db	A;Genetics: C84561 A;Map position: 1	A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; PMID:20083487; PMID:10617197
RESULT 11		
Qy	34 MNSS--BSKRTLTTSLA--WQPPEV-IQQYLSGGMCYDLDGCPWPYD1GPKDAKGL 86	Query Match 11.3%; Score 229; DB 2; Length 457;
Db	1 MNWNMIIQRRDFGDTILEDFEPPELDEVLYRXPQGYHGVDEGRPYVIERLGKVDA SKL 60	Best Local Similarity 31.2%; Pred. No. 1.e-11; Mismatches 83; Indels 20; Gaps 5;
Qy	87 LFSASKQDILRTMRECEILLLOCAHOTTKL-----GRKVETITTYDC8GLGLKHLW 139	Qy 31 SGSMWSSESK-----RTLTTSLAQQPPEVIOQYLGSQGMCGYDLDGCPWPYD1GPKDA 83 Db 96 TNQMWSDLRKRKEFGADTVMEDDEFPEKIDEVLYKYPQGHGVDKGRPYVTERLGQYD 155
Db	61 MQVTILEYLRYHVKEFFKTI-----TVKFPACCIAKRHIDSSTTLDVQGLGXNFT 114	Qy 84 KGLFSASKQDILRTMRECEILLLOCAHOTTKLGRKVETITTYDC8GLGLKHLW 139 Db 156 TKLMQVTTMDRYVNTVWMEFERTFNFVKFPACTIAK-----HIDQSITLIDVQGVGLNEN 212
Qy	140 KPAVEAYGEFLCMFEENYPETIKRLFIVVKAPLKFVPPAVYLNLPKFLSEDTRKIMVILGAN 199	Qy 140 KPAVEAYGEFLCMFEENYPETIKRLFIVVKAPLKFVPPAVYLNLPKFLSEDTRKIMVILGAN 199
Db	115 KTARDLITIQOKLDSNDNPETLHRMFINAGSGCFKLIWGTVRSPFLDKTVSKHVLGNKY 174	Db 213 KAARDLTRLQKVDGDNYPETLNRMFINASGSPRMWLNWTYKSFSLDPKTTAKIHLGNKY 272
Qy	200 KEVLLKHSISPDQVPEYGGTMTDP 224	Qy 200 KEVLLKHSISPDQVPEYGGTMTDP 224
Db	175 QNKLEMIDASQUPDFEFFSGTCAD 199	Db 214 KPAVEAYGEFLCMFEENYPETIKRLFIVVKAPLKFVPPAVYLNLPKFLSEDTRKIMVILGAN 199
RESULT 9		
Qy	T38768 probable sec14 cytosolic factor - fission yeast (Schizosaccharomyces pombe)	Qy 200 KEVLLKHSISPDQVPEYGGTMTDP 224
Db	C;Species: Schizosaccharomyces pombe	Db 214 KPAVEAYGEFLCMFEENYPETIKRLFIVVKAPLKFVPPAVYLNLPKFLSEDTRKIMVILGAN 199
Qy	C;Accession: T38768 #Sequence_revision 03-Dec-1999 #text_change 09-Jul-2004	Db 215 KARQLLTRLQKVDGDNYPETLNRMFINASGSPRMWLNWTYKSFSLDPKTTAKIHLGNKY 272
Db	R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.	Qy 200 KEVLLKHSISPDQVPEYGGTMTDP 224
Qy	Submitted to the EMBL Data Library, January 1996	A;Reference number: Z21810
Db	GB:AE002093; NID:94874285; PI	

Db	273	QSKULEI1DASELPFLGSCTCADNGGCMRSDKGPWNNDIMKRVNNGDHICSK--RS	329	Qy	35	WSSE-SKRTLTLTSLAWOPPEVQQYLSSGMCGYDLDGCPWYDIIGPKDAKGULFSASK 93
Qy	248	QVKQOYEVHSVQISPGSSHQVE 268		Db	120	WRKEFGVDTIMEDDFREIDEVLYKYYFQGYHSGVDKDRPVPVTERLGVDATKLMQVTID 179
Db	330	QADNAGENI--ISCGNNSAVE 348		Qy	94	DILRTRKRECE --LLIQCBAHQTTLGRKVETITIYDCEGLGLKHLWKPAVEAYGEF 149
		RESULT 11		Db	180	RYVKYHVAREFEXTNIKLPACSIAAKK--HIDQSTTILDVGQVGLKSFSKAARDLQLRI 236
Db	84539	hypothetical protein At2g16380 [imported] - Arabidopsis thaliana		Qy	150	LGMFEENYPETKLRLFVYKAPKLFPVAYNLKPFLSSTRKIMVGANYKEVLKHLHSP 209
C;Species:	Arabidopsis thaliana (mouse-ear cress)			Db	237	QKIDSDNPETUNRMFIINAGSFRLLWSTVKSFLDPKTTAKHVGLGNKYQSKELEIDS 296
C;Accession:	F84539			Qy	210	DQVPEVYGGTM-----DPD-----GNPKCKSK 232
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;	M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Talon, L.;			Db	297	NEUPEFLGGNCITCADCKGCGMRSPDGKPNNDPDKMVQNGEGRCPRK 342
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.	Nature 402, 761-768, 1999					
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	A;Reference number: A84420; MUID:20083487; PMID:10617197		RESULT 13			
A;Accession: F84539	A;Status: preliminary					
A;Molecule type: DNA						
A;Residues: 1-582 <STO>						
A;Cross-references: UNIPROT:Q9SIW3; UNIPARC:UPI000017A75C; GB:AE002093; NID:94544391; PI						
C;Genetics:						
A;Gene: At2g16380						
A;Map position: 2						
Query Match 10.8%; Score 218; DB 2; Length 582;						
Best Local Similarity 29.2%; Pred. No. 2.2e-10;						
Matches 59; Conservative 38; Mismatches 91; Indels 14; Gaps 3;						
Qy 34 MWSSESK-----RTTTLTSLAWQPPEVQQYLSSGMCGYDLDGCPWYDIIGPKDAKGL 86						
Db 104 MWSDMLQWRMDFGVDTIEDDFEEFIDQVLYKHYFQGYHSGVDKDRPVPVTERLGVDARDL 163						
Qy 87 LFSASKDQLLRTKRECELLLQ---ECAHQTTLGRKVETITIYDCEGLGLKHLWKPA 142						
Db 164 LQATIMDPRYKHYKEFKRKFPSCSAAAKK--HIDQSTTIFDQVGVLKRNENSA 220						
Qy 143 VEAYGEFLCMFEENYPETKLRLFVYKAPKLFPVAYNLKPFLSSTRKIMVGANYKEV 202						
Db 221 RELLORLKLIDNDNXPETLNRMFIINAGPFRLLWAPIKKFLDFKTTSKHVGLGNKYQPK 280						
Qy 203 LIKHSISPQVPEVYGGTMDD 224						
Db 281 LLEALDASELPYFFGCLCTRCAD 302						
RESULT 12						
Db	84602	hypothetical protein At2g21540 [imported] - Arabidopsis thaliana		Qy	38	ESKRTLTLTSLAWQPPEVQQYLSSGMCGYDLDGCPWYDIIG--PKD 82
C;Species:	Arabidopsis thaliana (mouse-ear cress)			Db	98	DSLRMLEKCLEWREEFKAELTEEDLGFXDLGRVAYKRGYDKEGHPCVNAVYVFKEKE 157
C;Accession:	E84602			Qy	83	AKGLLFASQK--DILRTRKRECELLLQCAHQTTLGRK-----VETITIYDCEG 132
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;	M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Talon, L.;			Db	158	MYERVFGDEEKLNFLRWRV-----QLERGYKMLHFKPGGNTSIIQYTDLKD 205
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.	Nature 402, 761-768, 1999			Qy	133	LGLKHLWKPAVEAYGEFLCMFEENYPETKLRLFVYKAPKLFPVAYNLKPFLSSTRKIK 191
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	A;Reference number: A84420; MUID:20083487; PMID:10617197			Db	206	MPKRELL---RVAQNQILSFQDNYPELVATKEINVPPYFSVYMSMFSPLFORTKSKF 261
A;Accession: E84602	A;Status: preliminary			Qy	192	IMVUGANCYKEVLKHLHISPDQPVYEGGTMDDP-- -GNPKCKSKINYGSDIPRKYYVRDQ 248
A;Molecule type: DNA				Db	262	VMSKEGNAETLYKPIRPEDIPVQYQGLSRPTDQNGPPKPASSFSIKG----- 310
A;Residues: 1-371 <STO>				Qy	249	VKQOYEHSVQTSRGSSSHQVEYILLPGCVLRLWQPMNSDGAADVGFGLPLKTYKNGERQRAGEM 308
A;Cross-references: UNIPROT:Q9SIKS; UNIPARC:UPI0000A24B9; GB:AE002093; NID:94567235; PI				Db	311	-----GEKVNQIEGEGEGATITWDVUGGMDEYS----- 341
C;Genetics:				Qy	309	TEVLPNQRYNHLIYPED-----GLTLCSDPGIVYVLRFDNTYSFHAKRV---N 353
A;Gene: At2g21540				Db	342	AEPVNAEAEYIAVVEKPKRMKATDEAVCNSTFTVEAGKLISDNTLs-RKGVAAVR 399
A;Map position: 2				Qy	354	PTV 356
Query Match 10.8%; Score 217 5; DB 2; Length 371;				Db	400	YTV 402
Best Local Similarity 28.3%; Pred. No. 1.3e-10;						
Matches 35; Conservative 35; Mismatches 96; Indels 31; Gaps 5;						

RESULT 14		Query Match 10.4%; Score 210; DB 2; Length 301;	
		Best Local Similarity 29.8%; Pred. No. 4..e-10;	
		Matches 57; Conservative 38; Mismatches 80; Indels 16; Gaps 5;	
T05278	hypothetical protein T4L20_160 - Arabidopsis thaliana		
C;Species: Arabidopsis thaliana (mouse-ear cress)			
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004			
C;Accession: T05278			
R;Berry, M.; Terryn, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; Deew, H.W.; Mayer, K.P.X.; Schueler, C.			
A;Submitted to the Protein Sequence Database, September 1998			
A;Reference number: Z15406			
A;Accession: T05278			
A;Molecule type: DNA			
A;Residues: 1..550 <BEV>			
A;Cross-references: UNIPROT:065682; UNIPARC:UPI00000A8340; EMBL:AL023094			
A;Experimental source: cultivar Columbia; BAC clone T4L20			
C;Genetics:			
A;Map Position: 4			
A;Introns: 7/1; 91/2; 124/3; 213/3; 239/3; 323/3; 353/3; 403/2; 524/3			
A;Note: T4L20_160			
F;90..298/Domain: cellular retinaldehyde-binding protein homology <CRB>			
Qy	10..6*; Score 214; DB 2; Length 560;		
Db	Best Local Similarity 28.7%; Pred. No. 4..5e-10;		
Matches 58; Conservative 35; Mismatches 95; Indels 14; Gaps 3;			
Qy	34 MWSE-----SKRTLTSLAWQPPEVIOYQVLGGMCGYDLDGCPWYDITGPDKAGL 86		
Db	106 MWSDMIQRKDFGADTTEDFEEIEDEVMKHYPOQTHGVDEKGPRYYTERGQIDANKL 165		
Qy	87 LFSDCKPLLTKMRECE---LLQBCAHQTQLGRKVETTIIYCEGGLKLHMKPA 142		
Db	166 LQYTTMDRYVKHVKEPEKTYKVFPSCSVAANK--HIDQSTTILDVGVLKNFSKA 222		
Qy	143 VDAYGEFLCMFRENEYPTKLRLFVVKAPKLFPVAYNIKPFILSEDTRKIMVLYGANKEV 202		
Db	223 REILQLRCKDNENYPTLNRMFIINAGSGFRLLWSTVSKFLDPKTAKIHLGNKYHSK 282		
Qy	203 IILKHISPDQVPEVYGGTMDPD 224		
Db	283 LIIEVIDASELPFFGGAECTED 304		
RESULT 15			
S57923	SEC14 protein - yeast (<i>Candida albicans</i>)		
C;Species: <i>Candida albicans</i>			
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 26-Feb-1998			
C;Accession: S57923; S72193			
R;Monteoliva, L.; Sanchez, M.; Pla, J.; Gil, C.; Nombela, C.			
A;Submitted to the EMBL Data Library, September 1994			
A;Description: Characterisation of the <i>Candida albicans</i> SEC14 homolog gene.			
A;Reference number: S57923			
A;Accession: S57923			
A;Status: Preliminary			
A;Molecule type: DNA			
A;Residues: 1..301 <MOX>			
A;Cross-references: UNIPARC:UPI0000177B92; EMBL:X81937			
R;Monteoliva, L.; Sanchez, M.; Pla, J.; Gil, C.; Nombela, C.			
Year 12, 1097-1105, 1996			
A;Title: Cloning of <i>Candida albicans</i> SEC14 gene homologue coding for a putative essential			
A;Reference number: S72193; PMID:97051600; PMID:8896277			
A;Accession: S72193			
A;Molecule type: DNA			
A;Residues: 1..301 <MOX>			
A;Cross-references: UNIPARC:UPI0000177B92; EMBL:X81937			
A;Note: the authors translated the codon CTG for residue 180 as Ser			
C;Genetics:			
A;Gene: SEC14			
C;Superfamily: cellular retinaldehyde-binding protein homology <CRB>			
F;59..866/Domain: cellular retinaldehyde-binding protein homology <CRB>			